



**European Patent Office**

Office européen des brevets

## A2

**EUROPEAN PATENT APPLICATION**

// A61K37/02

② Date of filing: 29.01.87

**Gloor, Sergio, Dr.**  
**Schauenburgerstrasse 26**  
**CH-4052 Basle (CH)**

(57)

(SIGNAL)  
Met Ser

74 81 163 222 307 458 576 646 712 858 915 1020 1215 ca.1500 (at 163)

Stu Stu Hae Pst Hae Stu Hc Hae Hc Pvu Pvu Hind III

0 250 706 530 932 1250 754 676

START OF SEQUENCE AT RESTRICTION SITE  
END OF SEQUENCE AT RESTRICTION SITE  
573 END OF CLEAN SEQUENCE AT POSITION 573

Stu = StuRI  
Hae = HaeIII  
Hc = HincII  
Pvu = PvuII

Bundesdruckerei Berlin

## Description

Neurite-promoting factor and process for the manufacture thereof

The invention relates to a neurite-promoting factor released by glial cells, to related proteins and fragments thereof retaining their neurite-promoting activity, to DNAs coding for the amino acid sequence of said neurite-promoting factor and fragments thereof, to hybrid vectors containing such DNAs, to hosts transformed with such a hybrid vector, to processes for the preparation of said DNAs, vectors and transformed hosts, to processes for the manufacture of said neurite-promoting factor, related proteins and its fragments, and to their use in the treatment of lesions in the nervous system.

Glial cells are thought to exert crucial regulatory functions during the development or following lesions of the nervous system. Knowledge about the nature of these glia-neuronal interactions requires the identification of macromolecules present in minute amount in the *in vivo* situation. Cultured rat glioma cells release a macromolecule which promotes neurite extension in neuroblastoma cells. This rat glia-derived neurite-promoting factor (GdNPF) has been purified and characterized [J. Guenther, H. Nick and D. Monard, EMBO J. 4, 1963-1966 (1985)]. It is a protein having an apparent molecular weight of 43 000 which causes both neurite extension and efficient inhibition of serine proteases such as urokinase, tissue plasminogen activator, thrombin and trypsin. The formation of a sodium dodecyl sulfate resistant complex between the proteases and rat GdNPF has been demonstrated by the same authors. Rat GdNPF inhibits the plasminogen activator activity released or associated with tumour cells and interferes with the migration of granule cell neurons taking place during the development of the cerebellum.

Such a neurite-promoting factor and related peptides, which cause neurite extension and inhibit serine proteases, are expected to promote nerve fiber regeneration following lesions in the nervous system and to interfere with the migration of normal and tumour cells. However, therapeutic applications of the known rat GdNPF to man are severely hampered by the expected antigenicity of rat GdNPF to man. This problem can be surmounted by the use of human GdNPF.

It is an object of the present invention to provide human GdNPF. The problem of industrial synthesis of GdNPF, fragments thereof retaining neurite-promoting activity and GdNPF-related peptides can be solved by the methods of recombinant DNA technology. A further object of the present invention is therefore to provide DNAs coding for GdNPF isolated from natural sources through establishment of a cDNA library of rat glioma cells, human glioma cells and optionally other glial cells, and a method of selection for DNA coding for GdNPF, and to provide DNA mutants and synthetic DNA sequences coding for GdNPF, GdNPF-related peptides or GdNPF fragments retaining neurite-promoting activity. These DNAs are introduced into hybrid vectors. Microorganisms or mammalian cell cultures transformed with such hybrid vectors will express GdNPF or fragments thereof. It is a further object of the present invention to provide such hybrid vectors, transformed hosts, a process of manufacture of GdNPF, GdNPF-related peptides and fragments thereof, pharmaceutical preparations containing GdNPF, GdNPF-related peptides and fragments thereof, and a method for the treatment of lesions in the nervous system with such compounds.

The invention relates to essentially pure human glia-derived neurite-promoting factor (GdNPF), related polypeptides and fragments thereof retaining neurite-promoting activity. These compounds cause both neurite extension and inhibition of serin proteases.

More specifically the invention relates to human GdNPF of the formula  
 X<sub>1</sub>-Ser-His-Phe-Asn-Pro-Leu-Ser-Leu-Glu-Glu-Leu-Gly-Ser-Asn-Thr-Gly- 16  
 Ile-Gln-Val-Phe-Asn-Gln-Ile-Val-Lys-Ser-Arg-Pro-His-Asp-Asn-Ile- 32  
 Val-Ile-Ser-Pro-His-Gly-Ile-Ala-Ser-Val-Leu-Gly-Met-Leu-Gln-Leu- 48  
 Gly-Ala-Asp-Gly-Arg-Thr-Lys-Lys-Gln-Leu-Ala-Met-Val-Met-Arg-Tyr- 64  
 Gly-Val-Asn-Gly-Val-Gly-Lys-Ile-Leu-Lys-Lys-Ile-Asn-Lys-Ala-Ile 80  
 Val-Ser-Lys-Lys-Asn-Lys-Asp-Ile-Val-Thr-Val-Ala-Asn-Ala-Val-Phe- 96  
 Val-Lys-Asn-Ala-Ser-Glu-Ile-Glu-Val-Pro-Phe-Val-Thr-Arg-Asn-Lys- 112  
 Asp-Val-Phe-Gly-Cys-Glu-Val-Arg-Asn-Val-Asn-Phe-Glu-Asp-Pro-Ala- 128  
 Ser-Ala-Cys-Asp-Ser-Ile-Asn-Ala-Trp-Val-Lys-Asn-Glu-Thr-Arg-Asp- 144  
 Met-Ile-Asp-Asn-Leu-Leu-Ser-Pro-Asp-Leu-Ile-Asp-Gly-Val-Leu-Thr- 160  
 Arg-Leu-Val-Leu-Val-Asn-Ala-Val-Tyr-Phe-Lys-Gly-Leu-Trp-Lys-Ser- 176  
 Arg-Phe-Gln-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe-Val-Ala-Ala-Asp- 192  
 Gly-Lys-Ser-Tyr-Gln-Val-Pro-Met-Leu-Ala-Gln-Leu-Ser-Val-Phe-Arg- 208  
 Cys-Gly-Ser-Thr-Ser-Ala-Pro-Asn-Asp-Leu-Trp-Tyr-Asn-Phe-Ile-Glu- 224  
 Leu-Pro-Tyr-His-Gly-Glu-Ser-Ile-Ser-Met-Leu-Ile-Ala-Leu-Pro-Thr- 240  
 Glu-Ser-Ser-Thr-Pro-Leu-Ser-Ala-Ile-Ile-Pro-His-Ile-Ser-Thr-Lys- 256  
 Thr-Ile-Asp-Ser-Trp-Met-Ser-Ile-Met-Val-Pro-Lys-Arg-Val-Gln-Val- 272  
 Ile-Leu-Pro-Lys-Phe-Thr-Ala-Val-Ala-Gln-Thr-Asp-Leu-Lys-Glu-Pro- 288  
 Leu-Lys-Val-Leu-Gly-Ile-Thr-Asp-Met-Phe-Asp-Ser-Ser-Lys-Ala-Asn- 304  
 Phe-Ala-Lys-Ile-Thr-X<sub>2</sub>-Ser-Glu-Asn-Leu-His-Val-Ser-His-Ile-Leu- 320  
 Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala-Ser-Ala- 336  
 Ala-Thr-Thr-Ala-Ile-Leu-Ile-Ala-Arg-Ser-Ser-Pro-Pro-Trp-Phe-Ile- 352  
 Val-Asp-Arg-Pro-Phe-Leu-Phe-Phe-Ile-Arg-His-Asn-Pro-Thr-Gly-Ala- 368

Val-Leu-Phe-Met-Gly-Gln-Ile-Asn-Lys-Pro 378

(I),

optionally glycosylated, wherein Cys is optionally in the disulfide form, X<sub>1</sub> is hydrogen, acyl, for example formyl or alkanoyl, e.g. palmitoyl, myristoyl or lower alkanoyl, such as acetyl or propionyl, the peptide residue of the formula

-19                      -15                      -10                      -5  
Met-Asn-Trp-His-Leu-Pro-Leu-Phe-Leu-Leu-Ala-Ser-Val-Thr-Leu-Pro-Ser-

-1  
Ile-Cys-

(II),

or a fragment of the residue of formula II comprising between 1 and 18 amino acids from the carboxyl end, optionally in acylated form, and X<sub>2</sub> is Arg or Thr-Gly, to related polypeptides retaining neurite-promoting activity, wherein one or more, especially one, two, three or four, single amino acids in the compound of the formula I are replaced by other amino acids, and to fragments of the compound of formula I comprising at least 10 consecutive amino acids selected from the amino acid chain between the amino acid 29 and amino acid 378 and optionally one or more, e.g. one, two or three other amino acids.

The GdNPF of formula I may be glycosylated or devoid of carbohydrate residues. Typically, a glycosylated GdNPF of formula I contains one or more carbohydrate residues, e.g. N-acetylglucosamine or an oligosaccharide containing N-acetylglucosamine N-glycosidically linked to an asparagine (Asn) residue and/or N-acetylgalactosamine or an oligosaccharide containing N-acetylgalactosamine O-glycosidically linked to a serine (Ser) or threonine (Thr) residue.

It is understood that in the GdNPF of formula I the cysteine residues may be in the reduced form as shown or in the oxidized, i.e. disulfide form giving rise to S-S-bridges, preferably intramolecular S-S-bridges between any two Cys residues in the formula I.

Acyl X<sub>1</sub> may be any acyl group found in native proteins. Particularly, acyl X<sub>1</sub> is lower alkanoyl, e.g. acetyl, or formyl, preferably acetyl.

The peptide residue X<sub>1</sub> of the formula II is a signal peptide. The GdNPF as formed in the ribosomes contains the whole peptide residue X<sub>1</sub> of formula II. Post-translational processing then cuts off this signal peptide or part of it. The invention relates to the GdNPF of formula I, wherein X<sub>1</sub> is the peptide residue of the formula II or fragments of this residue as defined hereinbefore, particularly wherein X<sub>1</sub> is the fragment comprising the amino acids -18 to -1, Pro-Ser-Ile-Cys- (-4 to -1), Ser-Ile-Cys- (-3 to -1), Ile-Cys-, or Cys- only. The peptide residue of formula II or its fragments comprising between 1 and 18 amino acids from the carboxyl end may be acylated, e.g. acetylated or formylated, at the N-terminal.

R.W. Scott et al [J. Biol. Chem. 260, 7029-7034 (1985)] describe a polypeptide called protease nexin. This serine protease inhibitor is released from cultured human fibroblasts. Protease nexin is reported to have an apparent molecular weight of 43 000 and a N-terminal amino acid sequence of 28 amino acids identical to the 28 amino acids of the N-terminal of the GdNPF of formula I. However, there is clear evidence demonstrating that the published protein named protease nexin and the GdNPF of the invention are different compounds. Table 1 lists the amino acid composition of this known protein as estimated from a total amino acid analysis, and the amino acid composition of GdNPF of formula I wherein X<sub>1</sub> is hydrogen. Most remarkable differences are found in the number of the amino acids threonine (Thr), serine (Ser), glutamic acid and glutamine (Glu/Gln), proline (Pro), valine (Val) and isoleucine (Ile).

Table 1: Amino acid composition of protease nexin<sup>a)</sup> and GdNPF

5		Ala	Arg	Asp/Asn	Cys	Glu/Gln	Gly	His	Ile		
	nexin	29	16	44	8	34	25	8	24		
10	GdNPF	28	15 or 14	41	3	26	18 or 19	8	31		
		Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val
15	nexin	32	28	9	17	13	43	34	n.d.	4	27
	GdNPF	31	29	10	19	21	33	21 or 22	5	5	34

a) R.W. Scott et al., J.Biol.Chem. 260, 7029 (1985)

n.d. = not determined

The invention comprises also GdNPF-related polypeptides retaining neurite-promoting activity, e.g. a compound of the formula I, wherein one or more single amino acids are replaced by other amino acids. Such related polypeptides may be formed by spontaneous or chemically-induced mutations at the DNA level or by replacement of amino acids by chemical synthesis. Such related polypeptides comprise also hybrid polypeptides consisting of fused fragments of GdNPF derived from different animal species including human GdNPF.

Fragments of the invention are e.g. large fragments of the compound of formula I, wherein only few amino acids at the N-terminal are missing, for example fragments comprising amino acids 2 to 378, 3 to 378, 4 to 378, 5 to 378, 6 to 378, or 7 to 378, or small fragments of 10 to 50 amino acids comprising amino acids <sup>310</sup>Arg and <sup>311</sup>Ser and/or amino acids <sup>345</sup>Arg and <sup>346</sup>Ser and optionally other amino acids, combinations known to be essential parts of serine protease substrates. Other preferred fragments involve those regions showing considerable homology with antithrombin-III or  $\alpha$ 1-antitrypsin, e.g. fragments comprising amino acids selected from the amino acid chain 72 to 96, 134 to 146, 159 to 195, and 314 to 378, and optionally one or more, e.g. one, two or three other amino acids. Particularly preferred are the fragment consisting of 14 amino acids between amino acid 321 and 334, i.e. the fragment of the formula Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala, the fragment consisting of 13 amino acids between amino acids 322 and 334 and an additional histidine residue at the N-terminal, i.e. the fragment of the formula His-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala, the fragment consisting of 10 amino acids between amino acid 345 and 354 and an additional -Ser-Phe residue at the carboxy terminal, i.e. the fragment of the formula Arg-Ser-Ser-Pro-Pro-Trp-Phe-Ile-Val-Asp-Ser-Phe, and the fragment consisting of 14 amino acids between amino acid 175 and 188, i.e. the fragment of the formula Lys-Ser-Arg-Phe-Gly-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe.

The human GdNPF, related peptides and fragments thereof can be prepared by isolation from cells producing the desired compound or by synthesis by condensation reactions.

For example, human GdNPF may be obtained by culturing glioma cells or other glial cells producing it in suitable media, e.g. minimum essential medium, Dulbecco's modified Eagle medium, RPMI 1640 medium and the like, optionally supplemented with whole serum, e.g. fetal calf serum and/or growth-stimulating compounds, mitogens, antibiotics and other supplements. The desired GdNPF is isolated and purified by usual methods such as those discussed hereinbelow.

It is also possible to synthesize human GdNPF, related peptides and particularly fragments thereof by chemical methods, e.g. by condensation reactions as described in M. Bodanszky, Principles of Peptide Synthesis, Springer-Verlag 1984. Fragments are synthesized e.g. by a solid-phase method, wherein a N-protected amino acid is coupled to a suitable resin, the protecting group is removed, a second N-protected amino acid is condensed with the amino group of the first amino acid, the cycle of deprotection/condensation with the next N-protected amino acid is repeated until the peptide residue of the desired composition is complete, and finally this peptide residue is cleaved from the resin and deprotected. Suitable resins, protecting groups, condensation reagents and reaction conditions are well known in the art.

In particular, human GdNPF, related peptides and fragments thereof can be prepared by recombinant DNA technique comprising, for example, culturing a transformed host under conditions which allow expression of the heterologous polypeptide and isolating the desired compound. More specifically, the desired compounds

are prepared by

- a) isolating a DNA coding for GdNPF or a fragment thereof from a cDNA library of glial cells or a genomic DNA library and optionally mutating it, or chemically synthesizing such a DNA,
- b) incorporating the DNA into an appropriate expression vector,
- c) transferring the obtained hybrid vector into a recipient host,
- d) selecting the transformed host from untransformed hosts, e.g. by culturing under conditions under which only the transformed host survives,
- e) culturing the transformed host under conditions which allow expression of the heterologous polypeptide, and
- f) isolating the human GdNPF, related peptide, or fragment thereof.

The steps involved in the preparation of these peptides by recombinant DNA technique will be discussed in more detail hereinbelow.

For the preparation of human GdNPF, the cDNA library of step a) is preferentially derived from human glioma cells, e.g. from the human glioma cell line LN-340, which has been deposited at the "Collection Nationale de Cultures de Microorganismes", Institut Pasteur, Paris, on February 5, 1986 under the number I-518. A genomic DNA library of step a) may be prepared from human placenta or human fetal liver cells. For the preparation or related peptides, e.g. rat GdNPF, other glial cells, e.g. rat glioma cells, in particular C6 rat glioma cells, are used to prepare a cDNA library.

The invention relates also to DNAs coding for glia-derived neurite-promoting factor (GdNPF), e.g. DNAs coding for human GdNPF or for rat GdNPF, to mutants thereof, e.g. DNAs wherein one or more, especially one, two, three or four, nucleotides are mutated, to DNAs coding for related polypeptides retaining neurite-promoting activity, and to fragments of such DNA comprising at least 15 nucleotides. It is understood that such DNAs are single-stranded or double-stranded.

In particular, the invention concerns a DNA coding for human GdNPF, of the formula

$$Z_1-Y_{13}-Y_3-Y_{18}-Y_9-Y_{11}-Y_{15}-Y_{11}-Y_{14}-Y_{11}-Y_{11}-Y_{11}-Y_{16}-Y_{20}-Y_{17}-Y_{11}-Y_{15}-Y_{16}-Y_{10}-Y_5-Y_{18}-Y_9-Y_{14}-Y_3-Y_{15}-Y_{11}-Y_{18}-Y_{11}-Y_7-Y_7-Y_{11}-Y_8-Y_{16}-Y_3-Y_{17}-Y_8-Y_{10}-Y_6-Y_{20}-Y_{14}-Y_3-Y_6-Y_{10}-Y_{20}-Y_{12}-Y_{18}-Y_2-Y_{16}-Y_9-Y_4-Y_3-Y_{10}-Y_{20}-Y_{10}-Y_{18}-Y_{15}-Y_9-Y_6-Y_{10}-Y_{11}-Y_{16}-Y_{20}-Y_{11}-Y_8-Y_{13} \quad -Y_{11}-Y_6-Y_{11}-Y_8-Y_{11}-Y_4-Y_8-Y_2-Y_{17}-Y_{12}-Y_{12}-Y_6-Y_{11}-Y_{11}-Y_{13}-Y_{20}-Y_{13}-Y_2-Y_{19}-Y_8-Y_{20}-Y_3-Y_8-Y_{20}-Y_8-Y_{12}-Y_{10}-Y_{11}-Y_{12}-Y_{12}-Y_{10}-Y_3-Y_{12}-Y_{11}-Y_{10}-Y_{20}-Y_{18}-Y_{12}-Y_{12}-Y_3-Y_{12}-Y_4-Y_{10}-Y_{20}-Y_{17}-Y_{20}-Y_{11}-Y_3-Y_{11}-Y_{20}-Y_{14}-Y_{20}-Y_{12}-Y_3-Y_{11}-Y_{16}-Y_7-Y_{10}-Y_7-Y_{20}-Y_{15}-Y_{14}-Y_{20}-Y_{17}-Y_2-Y_3-Y_{12}-Y_4-Y_{20}-Y_{14}-Y_6-Y_5-Y_7-Y_{20}-Y_2-Y_3-Y_{20}-Y_3-Y_{14}-Y_7-Y_4-Y_{15}-Y_{11}-Y_{16}-Y_{11}-Y_6-Y_4-Y_{16}-Y_{10}-Y_3-Y_{11}-Y_{18}-Y_{20}-Y_{12}-Y_3-Y_7-Y_{17}-Y_2-Y_4-Y_{13}-Y_{10}-Y_4-Y_3-Y_{11}-Y_{11}-Y_{16}-Y_{15}-Y_4-Y_{11}-Y_{10}-Y_4-Y_8-Y_{20}-Y_{11}-Y_{17}-Y_2-Y_{11}-Y_{20}-Y_{11}-Y_{20}-Y_3-Y_{11}-Y_{20}-Y_{18}-Y_{14}-Y_{12}-Y_6-Y_{11}-Y_{18}-Y_{12}-Y_{16}-Y_2 \quad -Y_{14}-Y_6-Y_{15}-Y_7-Y_3-Y_{17}-Y_{12}-Y_{12}-Y_2-Y_{17}-Y_{14}-Y_{20}-Y_{11}-Y_{11}-Y_4-Y_8-Y_{12}-Y_{16}-Y_{19}-Y_6-Y_{20}-Y_{15}-Y_{13}-Y_{11}-Y_{11}-Y_6-Y_{11}-Y_{16}-Y_{20}-Y_{14}-Y_2-Y_5-Y_8-Y_{16}-Y_{17}-Y_{18}-Y_{11}-Y_{15}-Y_3-Y_4-Y_{11}-Y_{18}-Y_{19}-Y_3-Y_{14}-Y_{10}-Y_7-Y_{11}-Y_{15}-Y_{19}-Y_9-Y_8-Y_7-Y_{16}-Y_{10}-Y_{16}-Y_{13}-Y_{11}-Y_{10}-Y_{11}-Y_{15}-Y_{17}-Y_7-Y_{16} \quad -Y_{18}-Y_{17}-Y_{15}-Y_{11}-Y_{16}-Y_{11} \quad -Y_{10}-Y_{10}-Y_{15}-Y_9-Y_{10}-Y_{16}-Y_{17}-Y_{12}-Y_{17}-Y_{10}-Y_4-Y_{16}-Y_{18}-Y_{13}-Y_{16}-Y_{10}-Y_{13}-Y_{20}-Y_{15}-Y_{12}-Y_2-Y_{20}-Y_6-Y_{20}-Y_{10}-Y_{11}-Y_{15}-Y_{12}-Y_{14}-Y_{17}-Y_{11}-Y_{20}-Y_{11}-Y_6-Y_{17}-Y_4-Y_{11}-Y_{12}-Y_7-Y_{15}-Y_{11}-Y_{12}-Y_{20}-Y_{11}-Y_8-Y_{10}-Y_{17}-Y_4-Y_{13}-Y_{14}-Y_4-Y_{16}-Y_{18}-Y_{12}-Y_{11}-Y_3-Y_{14}-Y_{11}-Y_{12} \quad -Y_{10}-Y_{17}-Y_{22}-Y_{16}-Y_7-Y_3-Y_{11}-Y_9-Y_{20}-Y_{16}-Y_9-Y_{10}-Y_{11}-Y_6-Y_{12}-Y_{11}-Y_{12}-Y_{10}-Y_7-Y_{20}-Y_{16}-Y_7-Y_4-Y_8-Y_{17}-Y_{12}-Y_{11}-Y_{16}-Y_{11}-Y_{11}-Y_{17}-Y_{17}-Y_{11}-Y_{10}-Y_{11}-Y_{10}-Y_{11}-Y_2-Y_{16}-Y_{16}-Y_{15}-Y_{15}-Y_{18}-Y_{14}-Y_{10}-Y_{20}-Y_4-Y_2-Y_{16}-Y_{14}-Y_{11}-Y_{14}-Y_{14}-Y_{10}-Y_2-Y_9-Y_3-Y_{15}-Y_{17}-Y_8-Y_{11}-Y_{20}-Y_{11}-Y_{14}-Y_{13} \quad -Y_8-Y_6-Y_{10}-Y_3-Y_{12}-Y_{15}-Y_{21}-Z_2$$

(III),

wherein

- $Y_1$  codes for alanine (Ala) and is GCT, GCC, GCA or GCG,  
 $Y_2$  codes for arginine (Arg) and is CGT, CGC, CGA, CGG, AGA or AGG,  
 $Y_3$  codes for asparagine (Asn) and is AAT or AAC,  
 $Y_4$  codes for aspartic acid (Asp) and is GAT or GAC,  
 $Y_5$  codes for cysteine (Cys) and is TGT or TGC,  
 $Y_6$  codes for glutamine (Gln) and is CAA or CAG,  
 $Y_7$  codes for glutamic acid (Glu) and is GAA or GAG,  
 $Y_8$  codes for glycine (Gly) and is GGT, GGC, GGA or GGG,  
 $Y_9$  codes for histidine (His) and is CAT or CAC,  
 $Y_{10}$  codes for isoleucine (Ile) and is ATT, ATC or ATA,  
 $Y_{11}$  codes for leucine (Leu) and is TTA, TTG, CTT, CTC, CTA or CTG,  
 $Y_{12}$  codes for lysine (Lys) and is AAA or AAG,  
 $Y_{13}$  codes for methionine (Met) and is ATG,  
 $Y_{14}$  codes for phenylalanine (Phe) and is TTT or TTC,  
 $Y_{15}$  codes for proline (Pro) and is CCT, CCC, CCA or CCG,  
 $Y_{16}$  codes for serine (Ser) and is TCT, TCC, TCA, TCG, AGT or AGC,  
 $Y_{17}$  codes for threonine (Thr) and is ACT, ACC, ACA or ACG,  
 $Y_{18}$  codes for tryptophan (Trp) and is TGG,  
 $Y_{19}$  codes for tyrosine (Tyr) and is TAT or TAC,  
 $Y_{20}$  codes for valine (Val) and is GTT, GTC, GTA or GTG,  
 $Y_{21}$  is a stop codon TAA, TAG or TGA,  $Y_{22}$  is  $Y_2$  or  $Y_{17}-Y_8$ ,  
 $Z_1$  is a flanking DNA residue of 12 nucleotides or more containing a promoter sequence, and  
 $Z_2$  is absent or a flanking DNA residue of one or more nucleotides and  $Z_1$  and  $Z_2$  are optionally linked,

a double-stranded DNA consisting of a DNA of formula III and of a complementary DNA thereto, wherein adenine (A) combines with thymine (T) and vice versa, and guanine (G) combines with cytosine (C) and vice versa, that complementary DNA itself, a mutant thereof, wherein one or more, especially one, two, three or four nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.

5 Especially, the invention concerns the cDNA coding for human GdNPF, of the formula

MetAsnTrpHisLeuProLeuPheLeuLeuAlaSer    -8

10 Z<sub>3</sub>-CGGTCGTCCTTGGTGGGAAGTAACCATGAAGTGGCATCTCCCCCTCTTCCTCTTGGCCTCT    60

-1 1

ValThrLeuProSerIleCysSerHisPheAsnProLeuSerLeuGluGluLeuGlySerAsn    14

15 GTGACGCTGCCTTCCATCTGCTCCCACTTCAATCCTCTGTCTCTCGAGGAAGTGGCTCCAAC    123

ThrGlyIleGlnValPheAsnGlnIleValLysSerArgProHisAspAsnIleValIleSer    35

20 ACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCCCTCATGACAACATCGTGATCTCT    186

ProHisGlyIleAlaSerValLeuGlyMetLeuGlnLeuGlyAlaAspGlyArgThrLysLys    56

25 CCCCATGGGATTGCGTCGGTCTCTGGGGATGCTTCAGCTGGGGGCGGACGGCAGGACCAAGAAG    249

GlnLeuAlaMetValMetArgTyrGlyValAsnGlyValGlyLysIleLeuLysLysIleAsn    77

30 CAGCTCGCCATGGTGATGAGATACGGCGTAAATGGAGTTGGTAAATATTAAAGAAGATCAAC    312

LysAlaIleValSerLysLysAsnLysAspIleValThrValAlaAsnAlaValPheValLys    98

35 AAGGCCATCGTCTCCAAGAAGAATAAAGACATTGTGACAGTGGCTAACGCCGTGTTTGTTAAG    375

40

45

50

55

60

65

AsnAlaSerGluIleGluValProPheValThrArgAsnLysAspValPheGlnCysGluVal	119	
AATGCCTCTGAAATTGAAGTGCCTTTTGTACAAGGAACAAAGATGTGTCCAGTGTGAGGTC	438	
ArgAsnValAsnPheGluAspProAlaSerAlaCysAspSerIleAsnAlaTrpValLysAsn	140	5
CGGAATGTGAACCTTTGAGGATCCAGCCTCTGCCTGTGATTCCATCAATGCATGGGTAAAAAC	501	
GluThrArgAspMetIleAspAsnLeuLeuSerProAspLeuIleAspGlyValLeuThrArg	161	10
GAAACCAGGGATATGATTGACAATCTGCTGTCCCAGATCTTATTGATGGTGTGCTCACCAGA	564	
LeuValLeuValAsnAlaValTyrPheLysGlyLeuTrpLysSerArgPheGlnProGluAsn	182	15
CTGGTCCTCGTCAACGCAGTGTATTTCAAGGGTCTGTGAAATCACGGTTCCAACCCGAGAAC	627	
ThrLysLysArgThrPheValAlaAlaAspGlyLysSerTyrGlnValProMetLeuAlaGln	203	20
ACAAAGAAACGCACCTTCGTGGCAGCCGACGGGAAATCCTATCAAGTGCCAATGCTGGCCCAG	690	
LeuSerValPheArgCycGlySerThrSerAlaProAsnAspLeuTrpTyrAsnPheIleGlu	224	25
CTCTCCGTGTTCGGTGTGGGTCCACAAGTGCCCCCAATGATTTATGGTACAACCTTCATTGAA	753	
LeuProTyrHisGlyGluSerIleSerMetLeuIleAlaLeuProThrGluSerSerThrPro	245	30
CTGCCCTACCACGGGAAAGCATCAGCATGCTGATTGCACTGCCGACTGAGAGCTCCACTCCG	816	
LeuSerAlaIleIleProHisIleSerThrLysThrIleAspSerTrpMetSerIleMetVal	266	35
CTGTCTGCCATCATCCACACATCAGCACCAAGACCATAGACAGCTGGATGAGCATCATGGTG	879	
ProLysArgValGlnValIleLeuProLysPheThrAlaValAlaGlnThrAspLeuLysGlu	287	40
CCCAAGAGGGTGCAGGTGATCCTGCCCAAGTTCACAGCTGTAGCACAAACAGATTGGAAGGAG	942	
ProLeuLysValLeuGlyIleThrAspMetPheAspSerSerLysAlaAsnPheAlaLysIle	308	45
CCGCTGAAAGTTCTTGGCATTACTGACATGTTTGATTTCATCAAAGGCAAATTTGCAAAAATA	1005	
ThrX <sub>2</sub> -SerGluAsnLeuHisValSerHisIleLeuGlnLysAlaLysIleGluValSerGlu	329	50
ACAWGGTCAGAAAACCTCCATGTTTCTCATATCTTGCAAAAAGCAAAAATTGAAGTCAGTGAA	1068	
AspGlyThrLysAlaSerAlaAlaThrThrAlaIleLeuIleAlaArgSerSerProProTrp	350	55
GATGGAACCAAAGCTTCAGCAGCAACAACTGCAATTCTCATTGCAAGATCATCGCCTCCCTGG	1131	
		60
		65

PheIleValAspArgProPheLeuPhePheIleArgHisAsnProThrGlyAlaValLeuPhe 371  
 TTTATAGTAGACAGACCTTTTCTGTTTTTCATCCGACATAATCCTACAGGTGCTGTGTTATT 1194

5

MetGlyGlnIleAsnLysPro

ATGGGGCAGATAAACAAACCCTGAAGAGTATACAAAAGAAACCATGCAAAGCAACGACTACTT 1257

10

TGC-Z<sub>4</sub>

(IV),

15

wherein W is A or ACAG, X<sub>2</sub> is Arg or Thr-Gly and Z<sub>3</sub> and Z<sub>4</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-stranded DNA consisting of a DNA of formula IV and of a complementary DNA thereto, that complementary DNA itself, a mutant thereof, wherein one or more, especially one, two, three or four nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.

20

The invention relates also to a DNA which hybridizes with a DNA of formula IV or with a DNA complementary to the DNA of formula IV.

The invention further concerns the cDNA coding for rat GdNPF, of the formula

25

-1 1

MetAsnTrpHisPheProPhePheIleLeuThrThrValThrLeuSerSerValTyrSer 1

Z<sub>5</sub>-ATGAATTGGCATTTCCTTCTTCATCTTGACCACAGTGACTTTATCCTCTGTGTACTCC 60

30

GlnLeuAsnSerLeuSerLeuGluGluLeuGlySerAspThrGlyIleGlnValPheAsn 21

CAGCTCAACTCTCTGTCACTCGAGGAAGTGGCTCTGACACAGGGATCCAGGTTTCAAT 120

35

GlnIleIleLysSerGlnProHisGluAsnValValIleSerProHisGlyIleAlaSer 41

CAGATCATCAAATCACAGCCTCATGAGAACGTTGTCAATTTCTCCGCACGGGATTGCGTCC 180

40

45

50

55

60

65



IleLeuGlyMetLeuGlnLeuGlyAlaAspGlyArgThrLysLysGlnLeuSerThrVal	61	
ATCTTGGGCATGCTGCAGCTGGGGGCTGACGGCAGGACGAAGAAGCAGCTCTCAACGGTG	240	
MetArgTyrAsnValAsnGlyValGlyLysValLeuLysLysIleAsnLysAlaIleVal	81	5
ATGCGATACAATGTGAACGGAGCTCGGAAAAGTGCTGAAGAAGATCAACAAGGCTATAGTC	300	
SerLysLysAsnLysAspIleValThrValAlaAsnAlaValPheValArgAsnGlyPhe	101	10
TCCAAAAGAATAAAGACATAGTGACCGTGGCCAATGCTGTGTTGTCAGGAATGGCTTT	360	
LysValGluValProPheAlaAlaArgAsnLysGluValPheGlnCysGluValGlnSer	121	15
AAAGTGGAAGTGCCTTTTGCAGCAAGGAACAAAGAGGTGTTTCACTGTGAAGTACAGAGT	420	
ValAsnPheGlnAspProAlaSerAlaCysAspAlaIleAsnPheTrpValLysAsnGlu	141	20
GTGAACTTCCAGGACCCGGCCTCTGCTTGTGATGCCATCAATTTTGGGTCAAAAATGAG	480	
ThrArgGlyMetIleAspAsnLeuLeuSerProAsnLeuIleAspSerAlaLeuThrLys	161	25
ACGAGGGGCATGATTGACAACCTACTTTCCCCAAATCTGATCGATAGTGTCTTACCAA	540	
LeuValLeuValAsnAlaValTyrPheLysGlyLeuTrpLysSerArgPheGlnProGlu	181	30
CTGTCCTCGTTAACGCAGTGTATTTCAAGGGTTTGTGGAATCCCGGTTTCAACCTGAG	600	
AsnThrLysLysArgThrPheValAlaGlyAspGlyLysSerTyrGlnValProMetLeu	201	35
AACACGAAGAAACGGACCTTCGTGGCAGGTGATGGAAATCCTACCAAGTACCCATGCTA	660	
AlaGlnLeuSerValPheArgSerGlySerThrLysThrProAsnGlyLeuTrpTyrAsn	221	40
GCCCAGCTCTCCGTGTTCCGCTCTGGGTCTACCAAACCCCAATGGCTTATGGTACAAC	720	
PheIleGluLeuProTyrHisGlyGluSerIleSerMetLeuIleAlaLeuProThrGlu	241	45
TTCATTGAGCTACCTACCATGGTGAGAGCATCAGCATGTTGATCGCCCTGCCAACAGAG	780	
SerSerThrProLeuSerAlaIleIleProHisIleSerThrLysThrIleAsnSerTrp	261	50
AGCTCCACCCCACTGTCCGCCATCATCCCTCACATCAGTACCAAGACCATCAATAGCTGG	840	
MetAsnThrMetValProLysArgMetGlnLeuValLeuProLysPheThrAlaLeuAla	281	55
ATGAACACCATGGTACCCAAGAGGATGCAGCTGGTCCTGCCCAAGTTCACAGCTCTGGCA	900	
		60
		65

GlnThrAspLeuLysGluProLeuLysAlaLeuGlyIleThrGluMetPheGluProSer 301  
 CAAACAGATCTGAAGGAGCCACTGAAAGCCCTTGGCATTACTGAGATCTTTGAACCGTCA 960

5

LysAlaAsnPheAlaLysIleThrArgSerGluSerLeuHisValSerHisIleLeuGln 321  
 AAGGCAAATTTTGCAAAATAACAAGGTCAGAGAGCCTTCACGTCTCTCACATCTTGCAG 1020

10

LysAlaLysIleGluValSerGluAspGlyThrLysAlaAlaValValThrThrAlaIle 341  
 AAAGCAAAATTTGAAGTCAGCGAAGATGGGACCAAGCCGCAGTAGTGACAACCTGCAATC 1080

15

LeuIleAlaArgSerSerProProTrpPheIleValAspArgProPheLeuPheCysIle 361  
 CTAATTGCAAGGTCATCGCCTCCCTGGTTTATAGTAGACAGGCCCTTTCCTGTTCTGCATC 1140

20

ArgHisAsnProThrGlyAlaIleLeuPheLeuGlyGlnValAsnLysPro  
 CGACACAATCCACAGGTGCCATCTTGTTCTGGGGCAGGTGAACAAGCCCTGA-Z<sub>6</sub>

25

(V),

wherein Z<sub>5</sub> and Z<sub>6</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-stranded DNA consisting of a DNA of formula V and of a complementary DNA thereto, that complementary DNA itself, a mutant thereof, wherein one or more, especially one, two, three or four nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.

Furthermore, the invention concerns RNAs coding for human GdNPF of formula I or for rat GdNPF, mutants thereof, wherein one or more, especially one, two, three or four nucleotides are mutated, and fragments of such RNAs comprising at least 15 nucleotides, in particular a RNA of formula III, wherein the various Y have the meaning given hereinbefore except that RNA residues replace DNA residues and hence uridine (U) replaces deoxy-thymidine (T), especially a RNA of formula IV and a RNA of formula V, wherein U replaces T.

The DNAs coding for GdNPF, mutants thereof, DNAs coding for related polypeptides retaining neurite-promoting activity and fragments of such DNA can be prepared, for example, by culturing a transformed host and isolating the desired DNA therefrom, or by chemical synthesis through nucleotide condensation.

In particular, such DNAs can be prepared, for example, by

- a) isolating poly(A) messenger RNA (mRNA) from glial cells, optionally enriching mRNA coding for GdNPF or fragments thereof and preparing single-stranded DNA complementary to that mRNA and therefrom double-stranded complementary DNA (ds cDNA), or
- b) isolating genomic DNA from suitable cells, e.g. placental or fetal liver cells, and selecting the desired DNA using a DNA probe, and
- c) incorporating ds cDNA of step a) or dsDNA of step b) into an appropriate expression vector,
- d) transforming an appropriate host with the obtained hybrid vector,
- e) selecting the transformed host which contains GdNPF DNA or fragments thereof from hosts containing no GdNPF DNA or fragments thereof, and
- f) isolating the desired DNA.

Polyadenylated messenger RNA is isolated from glial cells by known methods. Such methods involve, for example, homogenizing tissue in the presence of a detergent and a ribonuclease inhibitor, e.g. heparin, guanidinium isothiocyanate and mercaptoethanol, centrifuging the homogenate, precipitating mRNA from the supernatant by salt mixtures containing a magnesium salt, e.g. magnesium chloride, extracting the resuspended precipitate with suitable chloroform-phenol mixtures, optionally in the presence of detergents and/or cation chelating agents, and precipitating mRNA from the remaining aqueous, salt-containing phase with ethanol, isopropanol or the like. Otherwise, mRNA may be directly isolated by centrifuging in a cesium chloride gradient followed by ethanol precipitation. Preferentially, such precipitated poly(A) mRNA is further purified by chromatographic methods, e.g. affinity chromatography, for example chromatography on oligo(dT) cellulose or on oligo(dU) sepharose.

Glial cells used for the isolation of mRNA may be different origin. Preferred are glioma cells which can be expanded in culture, e.g. human glioma cells or rat glioma cells from established cell lines. Particularly preferred are cells from the human glioma cell line LN-340, which has been deposited at the "Collection

Nationale de Cultures de Microorganismes", Institut Pasteur, Paris, on February 5, 1986 under the number I-518.

Optionally, the mRNA isolated from glial cell is enriched in mRNA coding for neurite-promoting factor. This can be done, for example, by velocity fractionation or chromatographic fractionation of mRNA, translation of the fractions in suitable cells, e.g. in frog oocytes, or cell-free systems, e.g. reticulocyte extracts or wheat germ extracts, and screening of the obtained polypeptides for neurite-promoting activity or any other property which parallels neurite-promoting activity, e.g. protease inhibitory activity.

The screening of the obtained polypeptides is particularly effective using antibodies, e.g. polyclonal or monoclonal antibodies, in an immunoassay, for example radioimmunoassay, enzyme immunoassay or immunoassay with fluorescent markers. Such immunoassays and the preparation of polyclonal and monoclonal antibodies are well known in the art and are applied accordingly.

The screening can be done also on the stage of the messenger RNA, avoiding the additional step of translation, using a hybridization probe. Such hybridization probe may be a fully synthetic DNA consisting of at least 17 nucleotides or a DNA or DNA fragment isolated from a natural source or from a genetically engineered microorganism. For example, a plasmid containing a DNA coding for a GdNPF is multiplied in a suitable host, then linearized and the DNA isolated therefrom. After adding a suitable label to such DNA, e.g. a radioactive label, this DNA is used to screen for messenger RNA coding for a related GdNPF. Preferentially, a hybridization probe consisting of radioactively labelled DNA coding for rat GdNPF is used to screen a mRNA library for the presence of mRNA coding for human GdNPF.

The preparation of a single-stranded DNA from a mRNA template is well known in the art, as is the preparation of a double-stranded DNA from a single-stranded DNA. The mRNA template is incubated with a mix of deoxynucleoside triphosphates, optionally a radioactively labelled deoxynucleoside triphosphate (in order to be able to screen the result of the reaction), a primer sequence such as an oligo-dT residue hybridizing with the poly(A) tail of the messenger RNA and a suitable enzyme, e.g. a reverse transcriptase. After degradation of the template mRNA, the complementary DNA (cDNA) is incubated with a mix of deoxynucleoside triphosphates and a suitable enzyme as above to give a double-stranded DNA. Suitable enzymes are a reverse transcriptase, the Klenow fragment of *E. coli* DNA polymerase I or *T<sub>4</sub>* DNA polymerase. Optionally, the single-stranded DNA is first extended with a tail of like deoxynucleotides to allow the use of a primer sequence of complementary like deoxynucleotides, but the formation of dsDNA usually starts on spontaneous hairpin formation. Such dsDNA obtained as a result of hairpin formation is further processed with S1 nuclease which cuts the hairpin.

As an alternative to the preparation of cDNA from mRNA, genomic DNA may be isolated and screened for DNA coding for the desired polypeptide.

Genomic DNA is isolated from suitable tissue, preferably from human placenta or human fetal liver cells, according to methods known in the art. A genomic DNA library is prepared therefrom by digestion with suitable restriction endonucleases, e.g. AluI and HaeIII, and incorporation into  $\lambda$  charon phage, e.g.  $\lambda$  charon 4A, following established procedures. The genomic DNA library replicated on nitrocellulose membranes is screened with a DNA probe, e.g. a synthetic DNA probe of at least 17 nucleotides or a cDNA derived from mRNA coding for the desired polypeptide.

The incorporation of dsDNA prepared from mRNA or of genomic origin into an appropriate vector is well known in the art. Preferentially a suitable vector is cut and provided with tails of like deoxynucleosides. The dsDNA to be annealed then has to bear tails of complementary like deoxynucleotides, which is accomplished by incubation in the presence of the corresponding deoxynucleoside triphosphate and an enzyme such as terminal deoxynucleotidyl transferase. Otherwise, the dsDNA may be incorporated into the vector with the aid of linker oligonucleotides or else by blunt end ligation.

The transformation of an appropriate host with the obtained hybrid vector is well known in the art. For example, *E. coli* are conditioned for transformation by incubation in media containing calcium chloride, then treated with the hybrid vector. Transformed hosts are selected by a suitable marker, for example antibiotics resistance marker, e.g. tetracycline or ampicillin resistance.

The selection of the transformed hosts which contain GdNPF DNA or fragments thereof can be done by several methods. For example, plasmid DNA of transformed hosts is isolated and immobilized by usual methods, then hybridized with total mRNA from the glial cells initially used as a template for cDNA. Hybridizing RNA is eluted and translated *in vitro* as described hereinbefore. The polypeptides obtained on translation are screened for neurite-promoting activity, for protease inhibitory activity, or for immunoreaction with anti-GdNPF antibodies, and the transformed host containing the corresponding DNA selected. Otherwise, total DNA of transformed hosts is hybridized with DNA coding for GdNPF. For example, DNA of transformed hosts expected to code for human GdNPF is hybridized with DNA probes known to code for rat GdNPF.

The preparation of a DNA of the invention may also be performed by means of chemical synthesis. Suitable methods for the synthesis of DNA have been presented in summary form by S.A. Narang [Tetrahedron 39, 3 (1983)]. The known synthesis techniques allow the preparation of polynucleotides towards 40 nucleotides in length, in good yield, high purity and in a relatively short time. Suitably protected nucleotides are linked with one another by the phosphodiester method [K.L. Agarwal et al., Angew. Chem. 84, 489 (1972)] or the even more efficient phosphotriester method [C.B. Reese, Tetrahedron 34, 3143 (1972)], phosphite triester method [R.L. Letsinger et al., J. Am. Chem. Soc. 98, 3655 (1976)] or phosphoramidite method [S.L. Beaucage and M.H. Caruthers, Tetrahedron Letters 22, 1859 (1981)]. Simplification of the synthesis of the oligonucleotides and

polynucleotides is made possible by the solid phase method, in which the nucleotide chains are bound to a suitable polymer. Itakura et al. [J. Am. Chem. Soc. 103, 706 (1981)] use trinucleotides instead of individual nucleotides and link them by the phosphotriester method in the solid phase synthesis. A polynucleotide with up to 67 nucleotides can thus be prepared in a short time and with good yields. The actual double-stranded DNA can be built up enzymatically from chemically prepared overlapping oligonucleotides from both DNA strands, which are held together in the correct arrangement by base-pairing and are then chemically linked by the enzyme DNA ligase. Another possibility comprises incubating overlapping single polynucleotide sequences from the two DNA strands in the presence of the four required deoxynucleoside triphosphates with a DNA polymerase, for example DNA polymerase I, the Klenow fragment of polymerase I or T<sub>4</sub> DNA polymerase, or with AMV (avian myeloblastosis virus) reverse transcriptase. The two polynucleotide sequences are thereby held together in the correct arrangement by base-pairing and are supplemented with the required nucleotides by the enzyme to give a complete double-stranded DNA [S.A. Narang et al., Anal. Biochem. 121, 356 (1982)].

The invention further relates to hybrid vectors comprising a DNA coding for GdNPF, related peptides or fragments thereof operatively linked to an expression control sequence, and to processes for the preparation thereof.

The vector is selected depending on the host cells envisaged for transformation. Examples of suitable hosts are microorganisms, which are devoid of or poor in restriction enzymes or modification enzymes, such as yeasts, for example *Saccharomyces cerevisiae*, and strains of bacteria, in particular strains of *Escherichia coli*, for example *E. coli* X1776, *E. coli* HB 101, *E. coli* W3110, *E. coli* HB101/LM1035, *E. coli* JA221 or *E. coli* K12 strain 294, *Bacillus subtilis*, *Bacillus stearothermophilus*, *Pseudomonas*, *Haemophilus*, *Streptococcus* and others, and furthermore cells of higher organisms, in particular established human or animal cell lines. The above strains of *E. coli*, for example *E. coli* HB101 and *E. coli* JA221, and furthermore *Saccharomyces cerevisiae* are preferred as the host microorganism.

In principle, all vectors which replicate and express the GdNPF gene according to the invention in the chosen host are suitable. Examples of vectors which are suitable for the expression of the GdNPF in an *E. coli* strain are bacteriophages, for example derivatives of  $\lambda$  bacteriophages, or plasmids, such as, in particular, the plasmid ColE1 and its derivatives, for example pMB9, pSF2124, pBR317 or pBR322. The preferred vectors of the present invention are derived from plasmid pBR322. Suitable vectors contain a complete replicon and a marker gene, which allows to select and identify the hosts transformed with the expression plasmids on the basis of a phenotypical trait. Suitable marker genes impart to the host, for example, resistance towards heavy metals, antibiotics and the like. Furthermore, preferred vectors of the present invention contain, outside the replicon and marker gene regions, recognition sequences for restriction endonucleases, so that the GdNPF gene and, if appropriate, the expression control sequence can be inserted at these sites. The preferred vectors, the plasmid pBR322 and derived plasmids, e.g. pUC9, contain an intact replicon, marker genes which confer resistance towards tetracycline and ampicillin (*tet<sup>R</sup>* and *amp<sup>R</sup>*) and a number of unique recognition sites for restriction endonucleases, for example PstI (cleaves in the *amp<sup>R</sup>* gene, the *tet<sup>R</sup>* gene remains intact), BamHI, HindIII and SalI (all cleave in the *tet<sup>R</sup>* gene, the *amp<sup>R</sup>* gene remains intact), NruI and EcoRI.

Several expression control sequences can be used for regulation of the gene expression. In particular, expression control sequences of highly expressed genes of the host to be transformed are used. In the case of pBR322 as the hybrid vector and *E. coli* as the host microorganism, for example, the expression control sequences (which contain, *inter alia*, the promoter and the ribosomal binding site) of the lactose operon, tryptophan operon, arabinose operon and the like, the  $\beta$ -lactamase gene, the corresponding sequences of the phage  $\lambda$  N gene or the phage fd-coat protein gene and others, are suitable. Whilst the plasmid pBR322 already contains the promoter of the  $\beta$ -lactamase gene ( $\beta$ -lac gene), the other expression control sequences must be introduced into the plasmid.

Vectors which are suitable for replication and expression in yeast contain a yeast replication start and a selective genetic marker for yeast. Hybrid vectors which contain a yeast replication start, for example chromosomal autonomously replicating segment (ars), are retained extrachromosomally within the yeast cell after the transformation and are replicated autonomously. Furthermore, hybrid vectors which contain sequences homologous to the yeast 2 $\mu$  plasmid DNA can be used. Such hybrid vectors will get integrated by recombination into 2 $\mu$  plasmids already existing within the cell, or replicate autonomously. 2 $\mu$  sequences are particularly suitable for plasmids with a high transformation frequency and permit high copy numbers. The preferred yeast vector of the present invention is the plasmid pJDB207.

Suitable marker genes for yeasts are, in particular, those which impart antibiotic resistance to the host or, in the case of auxotrophic yeast mutants, genes which complement host lesions. Corresponding genes impart, for example, resistance towards the antibiotic cycloheximide or provide for prototrophy in an auxotrophic yeast mutant, for example the *URA3*, *LEU2*, *HIS3* or, in particular, *TRP1* gene. Yeast hybrid vectors furthermore preferably contain a replication start and a marker gene for a bacterial host, in particular *E. coli*, so that the construction and cloning of the hybrid vectors and their intermediates can take place in a bacterial host.

Expression control sequences which are suitable for expression in yeast are, for example, those of highly expressed yeast genes. Thus, the promoters of the *TRP1* gene, the *ADHI* or *ADHII* gene, acid phosphatase (*PHO3* or *PHO5*) gene, isocytocrome gene or a promoter involved with the glycolytic pathway, such as the promoter of the enolase, glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), 3-phosphoglycerate kinase (*PGK*), hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phos-

phoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase and glucokinase genes, can be used. Preferred vectors of the present invention contain promoters with transcriptional control, e.g. the promoters of the PHO5, ADHI1 and GAPDH genes, which can be turned on or off by variation of the growth conditions. For example, the PHO5 promoter can be repressed or derepressed solely by increasing or decreasing the concentration of inorganic phosphate in the medium.

Vectors suitable for replication and expression in mammalian cells are preferably provided with DNA from viral origin, e.g. from simian virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus 2, bovine papilloma virus (BPV), papovavirus BK mutant (BVK), or mouse or human cytomegalovirus (CMV). Preferably, such vectors contain an origin of replication and an antibiotics resistance gene for propagation in E. coli together with an eukaryotic transcription regulatory sequence. In particular, such so-called shuttle vectors may be constructed from a pBR322 E. coli plasmid and SV40 and/or CMV enhancer and promoter regions. For example, the plasmid may contain the enhancer unit of the mouse or human cytomegalovirus major immediate-early gene, the SV40 enhancer combined with the human  $\alpha$ -globin promoter, and/or in addition inducible promoters, such as the ones derived from the heat shock or metallothionein genes. Further it is also possible to utilize promoter or control sequences which are normally associated with the desired gene sequence. An origin of replication may be provided either by construction of the vector to include an exogenous origin, such as derived from SV40, other viral source or provided by the host cell chromosomal replication mechanism. If the vector is integrated into the host cell chromosome, the latter method is often more efficient.

In a preferred embodiment, the present invention relates to hybrid vectors capable of replication and phenotypical selection in a host strain comprising a promoter and a DNA encoding the GdNPF, related peptide or fragment thereof, said DNA being positioned together with transcription start and termination signals as well as translation start and stop signals in said hybrid vector under the control of said promoter such that in a transformed host it is expressed to produce the polypeptide.

The invention also relates to a process for the preparation of a transformed host, which comprises transforming a host with an expression vector containing a DNA of the invention regulated by an expression control sequence, and to the transformed hosts themselves.

Examples of suitable hosts are the above-mentioned microorganisms, such as strains of Saccharomyces cerevisiae, Bacillus subtilis and Escherichia coli. The transformation with the expression plasmids according to the invention is carried out, for example, as described in the literature, thus for S. cerevisiae [A. Hinnen et al., Proc. Natl. Acad. Sci. USA 75, 1929 (1978)], B. subtilis [Anagnostopoulos et al., J. Bacteriol. 81, 741 (1961)] and E. coli [M. Mandel et al., J. Mol. Biol. 53, 159 (1970)].

Accordingly, the transformation procedure of E. coli cells includes  $\text{Ca}^{2+}$ -pretreatment of the cells so as to allow DNA uptake, and incubation with the hybrid vector. The cells are transferred to a selective growth medium which allows separation of the transformed cells from the parent cells. Cells which do not contain the vector will not survive in such a medium. The transformation of yeast comprises, for example, the steps of (1) enzymatic removal of the yeast cell wall by means of glucosidases, (2) treatment of the obtained spheroplasts with the vector in the presence of polyethylene glycol and  $\text{Ca}^{2+}$ -ions and (3) regeneration of the cell wall by embedding the spheroplasts into agar. Preferably, the regeneration agar is prepared in a way to allow regeneration and selection of the transformed cells at the same time.

Further examples of suitable hosts are mammalian cells, e.g. COS-7 cells, Bowes melanoma cells, chinese hamster ovary (CHO) cells or embryonic lung cells L-132. The vectors are introduced into mammalian cells by transfection in the presence of helper compounds, e.g. diethylaminoethyl-dextran, dimethyl sulfoxide, glycerol, polyethylene glycol or the like, or as co-precipitates of vector DNA and calcium phosphate. Further suitable methods include direct microinjection of vector DNA into the cell nucleus and electroporation, i.e. introduction of DNA by a short electric pulse increasing the permeability of cell membranes. The subsequent selection of transfected cells can be done using a selection marker which is either covalently integrated into the expression vector or added as a separate entity. Selection markers include genes which confer resistance to antibiotics, e.g. G-418 (neomycin) or hygromycin, or genes which complement a genetic lesion of the host cell such as the absence of thymidine kinase or hyposanthine phosphoribosyl transferase.

The transformed host cells are cultured by methods known in the art in a liquid medium containing assimilable sources of carbon, nitrogen and inorganic salts.

Various sources of carbon can be used for culture of the transformed hosts according to the invention. Examples of preferred sources of carbon are assimilable carbohydrates, such as glucose, maltose, mannitol or lactose, or an acetate, which can be used either by itself or in suitable mixtures. Examples of suitable sources of nitrogen are amino acids, such as casaminoacids, peptides and proteins and their degradation products, such as tryptone, peptone or meat extracts; and furthermore yeast extracts, malt extract and also ammonium salts, for example ammonium chloride, sulfate or nitrate, which can be used either by themselves or in suitable mixtures. Inorganic salts which can also be used are, for example, sulfates, chlorides, phosphates and carbonates of sodium, potassium, magnesium and calcium.

The medium furthermore contains, for example, growth-promoting substances, such as trace elements, for example iron, zinc, manganese and the like, and preferably substances which exert a selection pressure and prevent the growth of cells which have lost the expression plasmid. Thus, for example, ampicillin is added to the medium if the expression plasmid contains an amp<sup>r</sup> gene. Such an addition of antibiotic substances also has the effect that contaminating antibiotic-sensitive microorganisms are destroyed. If a yeast strain which is auxotrophic in, for example, an essential amino acid, is used as the host microorganism, the plasmid

preferably contains a gene coding for an enzyme which complements the host defect. Cultivation of the yeast strain is performed in a minimal medium deficient in said amino acid.

Vertebrate cells are grown under tissue culture conditions using commercially available media optionally supplemented with growth-promoting substances and/or mammal sera. The cells are grown either attached to a solid support, e.g. a microcarrier or porous glass fibres, or free-floating in appropriate culture vessels.

Culturing is effected by processes which are known in the art. The culture conditions, such as temperature, pH value of the medium and fermentation time, are chosen so that a maximum titre of the polypeptide of the invention is obtained. Thus, an *E. coli* or yeast strain is preferably cultured under aerobic conditions by submerged culture with shaking or stirring at a temperature of about 20 to 40°C, preferably about 30°C, and a pH value of 4 to 8, preferably at about pH 7, for about 4 to 30 hours, preferably until maximum yields of the polypeptide of the invention are reached.

When the cell density has reached a sufficient value, the culture is interrupted and the polypeptide is isolated. If the polypeptide is fused with a suitable signal peptide sequence, it is excreted by the cell directly into the supernatant. Otherwise, the cells have to be destroyed, for example by treatment with a detergent, such as SDS, NP-40, Triton X or deoxycholic acid, or lysed with lysozyme, a similarly acting enzyme or with ultra-sound. If yeast is used as host microorganism the cell wall may be removed by enzymatic digestion with a glucosidase. Alternatively or additionally, mechanical forces, such as shearing forces (for example X-press, French press, Dyno mill) or shaking with glass beads or aluminium oxide, or alternating freezing, for example in liquid nitrogen, and thawing, for example to 30°C to 40°C, can be used to break the cells.

The cell supernatant or the solution obtained after centrifugation of the mixture obtained on breaking the cells, which contains proteins, nucleic acids and other cell constituents, is enriched in proteins, including the polypeptides of the invention, in a manner which is known *per se*. Thus, for example, most of the non-protein constituents are removed by polyethyleneimine treatment and the proteins, including the polypeptides of the invention, are precipitated, for example, by saturation of the solution with ammonium sulfate or with other salts. Otherwise, the cell supernatant or lysate may be directly pre-purified using chromatographic methods. Further purification steps include, for example, ultrafiltration, diafiltration, gel electrophoresis, chromatographic processes, such as ion exchange chromatography, size exclusion chromatography, high pressure liquid chromatography (HPLC), reversed phase HPLC, fast polypeptide liquid chromatography (FPLC) and the like separation of the constituents of the mixture according to molecular size by means of a suitable gel filtration column, dialysis, affinity chromatography, for example affinity chromatography using antibodies, especially monoclonal antibodies, and other processes known in the art.

The invention concerns furthermore GdNPF, related peptides and fragments thereof, whenever prepared according to the methods of the present invention.

The invention concerns especially the hybrid vectors, the transformed host cells, human GdNPF and the process for the preparation thereof as described in the Examples.

The neurite-promoting and serine protease-inhibiting properties of GdNPF, related peptides and fragments thereof according to the invention make these polypeptides useful for promoting nerve fiber regeneration following lesions in the nervous system, preferably in the form of pharmaceutical preparations that contain a therapeutically effective amount of the active ingredient optionally together or in admixture with inorganic or organic, solid or liquid, pharmaceutically acceptable carriers which are suitable preferably for parenteral administration.

Parenteral formulations are especially injectable fluids that are effective in various manners, such as intravenously, intramuscularly, intraperitoneally, intranasally, intradermally or subcutaneously. Such fluids are preferably isotonic aqueous solutions or suspensions which can be prepared before use, for example from lyophilized preparations which contain the active ingredient alone or together with a pharmaceutically acceptable carrier. The pharmaceutical preparations may be sterilized and/or contain adjuncts, for example preservatives, stabilizers, wetting agents and/or emulsifiers, solubilizers, salts for regulating the osmotic pressure and/or buffers. The present pharmaceutical preparations, which may, if desired, contain further pharmacologically valuable substances, are produced in a manner known *per se*, for example by means of conventional dissolving or lyophilizing processes, and contain from approximately 0.1 % to 100 %, especially from approximately 1 % to approximately 50 %, and in the case of lyophilisates up to 100 %, of the active ingredient.

The invention also concerns a method for producing a pharmaceutical preparation, characterized in that a pharmacologically active compound of the present invention is admixed with a pharmaceutically acceptable carrier.

The particular mode of administration and the dosage will be selected by the attending physician taking into account the particulars of the patient, the disease and the disease state involved. For instance, lesions of the nervous system are usually treated by daily or twice daily doses over a few days to a few weeks of 0.001 to 1 mg per kg body weight.

The following Examples serve to illustrate the present invention but should not be construed as a limitation thereof.

Figure 1 is a summary of the restriction and sequence analysis of a double-stranded complementary DNA coding from human GdNPF.

The abbreviations used in the Examples have the following meanings:  
bp base pairs

BSA bovine serum albumin	
cDNA complementary DNA	
cpm counts per min (radioactive decay)	
dA 2'-deoxyadenosine	
dATP 2'-deoxyadenosine triphosphate	
dC 2'-deoxycytidine	5
dCTP 2'-deoxycytidine triphosphate	
dG 2'-deoxyguanosine	
dGTP 2'-deoxyguanosine triphosphate	
DMEM Dulbecco's modified Eagle's medium	10
DNA deoxyribonucleic acid	
dNTP mixture of dATP, dCTP, dGTP and dTTP	
dpm disintegrations per min (radioactive decay)	
ds DNA double-stranded DNA	
dT 2'-deoxythymidine	15
DTT 1,4-dithiothreitol	
dTTP 2'-deoxythymidine triphosphate	
EDTA ethylenediamine-tetraacetic acid	
FCS fetal calf serum	
GdNPF glia-derived neurite promoting factor	20
Hepes N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid	
mRNA messenger RNA	
PBS phosphate buffered physiological saline	
Pipes piperazine-N,N'-bis(2-ethanesulfonic acid)	
PMSF phenylmethylsulfonyl fluoride	25
RNA ribonucleic acid	
rpm revolutions per min	
SDS sodium dodecyl sulfate	
TFA trifluoroacetic acid	
Tris tris(hydroxymethyl)aminomethane	30
tRNA transfer RNA	
The following buffer solutions and media are used:	
elution buffer 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.2 % SDS	
immunobuffer 50 mM Tris-HCl, pH 7.5, 1 mM EDTA, 150 mM NaCl, 0.1 % Tween-20®.	
Laemmli sample buffer 62.5 mM Tris-HCl, pH 6.8, 2 % SDS, 10 % glycerol, 5 % 2-mercaptoethanol, 0.001 % bromophenol blue.	35
LB-broth 1 % Bacto® tryptone (Difco), 0.5 % Bacto® yeast extract (Difco), 170 mM NaCl, adjusted to pH 7.5 with NaOH.	
RVT buffer 200 mM Tris-HCl, pH 8.3 at 42°C, 20 mM MgCl <sub>2</sub> , 280 mM KCl, 20 mM DTT.	
SSC buffer 15 mM sodium citrate, 150 mM NaCl, adjusted to pH 7.0 with NaOH.	40
TBE buffer 89 mM Tris (TRIZMA® base), 89 mM boric acid, 1 mM EDTA.	
TNE buffer 10 mM Tris-HCl, pH 8.0, 1 mM EDTA, 0.1 M NaCl.	
wash buffer 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl, 0.2 % SDS.	

**Example 1: Isolation of mRNA from rat C6 glioma cells** 45

Rat C6 glioma cells (ATCC No. CCL 107) are grown in 10 cm tissue culture dishes with 15 ml Dulbecco Modified Eagle Medium (Gibco) supplemented with 10 % fetal calf serum. 120 confluent dishes (about  $2.5 \times 10^7$  rat glioma cells per dish) are used to enrich mRNA as described by R. D. Palmiter [Biochemistry 13, 3606-3615 (1974)]. The mRNA fraction obtained by magnesium precipitation is further purified on oligo(dT) cellulose according to a method of M. Edmonds et al. [Proc. Natl. Acad. Sci. USA 68, 1336-1340 (1971)]. 50

**Example 2: Enriching mRNA for rat GdNPF**

600 µg poly(A) RNA from Example 1 (1 µg/µl) are heated for 5 min at 70°C, quickly chilled in ice water and loaded onto a 5-20 % linear sucrose gradient in 10 mM Hepes pH 7.5/1mM EDTA/100 mM NaCl and centrifuged for 23 h at 20000 rpm in a SW 27 rotor at 20°C. 20 fractions are collected and precipitated with ethanol at -20°C overnight. The mRNA is centrifuged for 20 min at 15000 rpm in a SS-34 rotor, washed once in 75 % ethanol and finally dissolved in water at a concentration of 1 µg/µl. 55

Individual fractions are assayed by injection into frog oocytes in the following way: 50 nl of each mRNA fraction tested is injected into 1 oocyte. Groups of 3 eggs containing the same mRNA are incubated in 100 µl Barth solution at 22°C for 24 h. The incubation medium is removed and assayed for protease inhibitory activity (which parallels GdNPF activity) in the casein degradation assay described by J. Guenther et al. [EMBO J. 4, 1963-1966 (1985)]. Briefly, a mixture of milk powder suspension, human urokinase, purified human plasminogen and the solution to be tested is incubated in a suitable buffer mixture, and the caseinolysis monitored by measuring the decrease in turbidity at 405 nm. The following results are obtained: 60

65

Fraction no.	% Inhibition of urokinase
1	not tested
2	not tested
5 3	not tested
4	5
5	not tested
6	5
7	not tested
10 8	4
9	not tested
10	3
11	35
15 12	28
13	75
14	57
15	38
16	12
20 17	not tested
18	6
19	not tested
20	5

The fractions 13 and 14 are pooled and used for cDNA synthesis (Example 3).

#### Example 3: Preparation of ds cDNA coding for rat GdNPF

Enriched mRNA coding for rat GdNPF of Example 2 is used as a template to prepare double-stranded DNA (ds DNA) essentially as described in the Maniatis handbook [T. Maniatis, E.F. Fritsch and J. Sambrook, "Molecular Cloning, a Laboratory Manual", Cold Spring Harbor Laboratory, 1982].

3.1 First strand synthesis: 100  $\mu$ l reaction mixture containing 100 mM Tris-HCl, pH 8.3 (at 42°C), 70 mM KCl, 10 mM MgCl<sub>2</sub>, 1 mM DTT, 1 mM of each dGTP, dCTP and dTTP, 0.4 mM dATP, 50  $\mu$ Ci  $\alpha$ -<sup>32</sup>P-dATP (Amersham, 3000 Ci/mmol), 50  $\mu$ g/ml oligo-dT (P-L Biochemicals), 100  $\mu$ g/ml mRNA (Example 2) and 50 units of avian myeloblastosis virus (AMV) reverse transcriptase (Stehelin, Basel, Switzerland) are incubated for 60 min at 42°C. The reaction is terminated by adjusting the solution to 10 mM EDTA. The mixture is hydrolyzed for 90 min at 52°C by adding 1M NaOH to 0.2 M final concentration. After neutralization with 1 M Tris-HCl, pH 8.0, and 1 M HCl, the reaction mixture is extracted with phenol/chloroform. The organic phase is back-extracted once with 10 mM Tris-HCl, pH 8.0/1 mM EDTA/100 mM NaCl. The pooled aqueous phases are applied on a Sephadex® G-50 column. 100  $\mu$ l fractions are collected and radioactivity monitored by Cerenkov counting [P.W.J. Rigby et al., J.Mol.Biol. 113, 237-251 (1977)]. cDNA containing fractions are pooled and precipitated with ethanol. The yield of single-stranded cDNA is 4.6  $\mu$ g. The size of the cDNA is 700-2000 nucleotides in length, as determined from its electrophoretic mobility in a 2% alkaline agarose gel in 30 mM NaOH/1 mM EDTA.

3.2 Second strand synthesis and S 1 digestion: The obtained cDNA is incubated in 100  $\mu$ l final volume of 100 mM Hepes, pH 6.9, 10 mM MgCl<sub>2</sub>, 2.5 mM DTT, 70 mM KCl, 0.5 mM of each dNTP, 5.8  $\mu$ Ci <sup>3</sup>H-dGTP, and 32 units of DNA polymerase (Klenov fragment, Boehringer Mannheim) for 150 min at 20°C. 16 units of the enzyme are added and the incubation continued for 60 min at 37°C. The reaction is terminated by adding EDTA to 10 mM. The mixture is extracted with phenol/chloroform and precipitated with ethanol. The resulting DNA is treated in a 100  $\mu$ l incubation mixture containing 250 mM NaCl, 50 mM sodium acetate pH 4.5, 1 mM ZnSO<sub>4</sub>, and 500 units/ml of S 1 endonuclease (Boehringer Mannheim) at 37°C for 30 min. The reaction is stopped by adding EDTA to 10 mM. After adding 1 M Tris-HCl, pH 8.0 to 100 mM, the reaction is extracted with phenol/chloroform. The cDNA is precipitated with ethanol at -70°C for 30 min. After centrifugation, the obtained ds cDNA is dissolved in 20  $\mu$ l of a solution of 50 mM Tris-HCl pH 7.4, 7 mM MgCl<sub>2</sub>, 1 mM DDT, 1 mM of each dNTP, and 1.5 units of the Klenov fragment. The reaction is incubated 30 min at 22°C and then stopped by adding EDTA to 10 mM. After extraction and passing through a Sephadex® CL-4B column in 10 mM Tris-HCl, pH 7.5/1 mM EDTA/300 mM NaCl, aliquots of cDNA containing fractions are assayed on a 2% agarose gel. Fractions with molecules > 600 bp are pooled, precipitated with ethanol and dissolved in 10 mM Tris HCl pH 7.5/1 mM EDTA. 0.6  $\mu$ g ds cDNA are obtained.

#### Example 4: Preparation of a vector containing ds cDNA coding for rat GdNPF from plasmid pBR 322 and transformation of E. coli HB 101 therewith

4.1. Preparation of ds cDNA with poly(dC) tails: 540 ng ds cDNA of Example 3 are incubated in 100  $\mu$ l solution containing 200 mM potassium cacodylate, pH 6.9, 1 mM CoCl<sub>2</sub>, 260 pmol <sup>3</sup>H-dCTP, and 6 units of terminal deoxynucleotidyl transferase (P-L Biochemicals) for 5 min at 37°C. To stop the reaction, EDTA is added to 10 mM. The mixture is extracted with phenol/chloroform, and the DNA precipitated with ethanol.



dC-tailed cDNA is stored at  $-20^{\circ}$  at 10 ng/ $\mu$ l.

4.2. Annealing of cut pBR 322 with poly(dG) tails to ds cDNA with poly(dC) tails and transformation of *E. coli* with the obtained vector: A mixture of 33 ng dC-tailed ds cDNA from Example 4.1 and 170 ng dG-tailed pBR322 (cut with Pst I, Boehringer Mannheim) in 200  $\mu$ l 10 mM Tris-HCl, pH 7.5/100 mM NaCl/1 mM EDTA is incubated 5 min at  $65^{\circ}$ C, 60 min at  $55^{\circ}$ C and then cooled to  $22^{\circ}$ C in a water bath. 40  $\mu$ l of this annealing mixture are added to 200  $\mu$ l of competent *E. coli* cells strain HB 101, which have been prepared for transformation as described in the Maniatis handbook. The mixture is kept on ice for 30 min and heated to  $42^{\circ}$  for 2 min, then treated with 1 ml of LB-broth and incubated at  $37^{\circ}$ C for 30 min. The mixture (200  $\mu$ l per plate) is spread of 8 cm agar plates containing LB-broth and 20  $\mu$ g/ml tetracycline. The plates are incubated at  $37^{\circ}$ C for 16 h. About 5000 tetracycline resistant colonies are obtained.

#### Example 5: Identification of clones containing DNA coding for rat GdNPF by hybridization selected translation

5.1. Hybridization: Individual colonies of Example 4 are grown to saturation in 200  $\mu$ l LB-broth containing 20  $\mu$ g/ml tetracycline. To obtain pools of 48 colonies, 50  $\mu$ l of each preculture are pipetted into 100 ml LB-broth containing 20  $\mu$ g/ml tetracycline. The pools are grown overnight. The DNA is isolated using the alkaline lysis method as described in the Maniatis handbook. The plasmid DNA is linearized with Eco RI, extracted and dissolved in 10 mM Tris-HCl, pH 7.5/1 mM EDTA at a concentration of 0.1  $\mu$ g/ $\mu$ l. 100  $\mu$ l of the solution are pipetted onto untreated Gene Screen $\oplus$  filters (New England Nuclear, 1 cm) in portions of 20  $\mu$ l and dried between each step. The filters are put 4 times for 1 min on 3 MM $\oplus$  paper (Whatman), which is soaked in 0.5 M NaOH/1.5 M NaCl. This procedure is repeated on 3 MM $\oplus$  paper soaked in 2 M Tris-HCl pH 7.4/double-concentrated SSC buffer, and finally on 3 MM $\oplus$  paper soaked only in double-concentrated SSC buffer. The filters are then gently agitated in double-concentrated SSC buffer and baked in a vacuum stove for 2 h at  $80^{\circ}$ C. Before use the filters are put in boiling water for 1 min.

Total RNA from rat C6 glioma cells (Example 1) is dissolved in 30 % formamide/20 mM Pipes, pH 7.5/500 mM NaCl/2 mM EDTA/0.4 % SDS at a concentration of 2 - 3 mg/ml. 130  $\mu$ l of this solution per filter is used for hybridization for 17 h at  $42^{\circ}$ C with gentle agitation. The filters are washed 10 times in SSC buffer/0.1 % SDS at  $60^{\circ}$ C and once in 5 mM Tris-HCl, pH 7.5/1 mM EDTA at  $60^{\circ}$ C. The hybridized RNA is eluted from the filters by two cycles of boiling in 200  $\mu$ l 5 mM KCl/10  $\mu$ g/ml tRNA (Boehringer Mannheim, phenol extracted) followed by quick freezing in dry ice-ethanol. After thawing, the eluates are pooled and the RNA precipitated with ethanol at  $-20^{\circ}$ C overnight. The precipitate is centrifuged and washed in 75 % ethanol. The poly(A) RNA obtained from each pool is dissolved in 4  $\mu$ l water and used for in vitro translation and immunoprecipitation with anti-GdNPF antibodies.

5.2. In vitro translation in the rabbit reticulocyte lysate: Rabbit reticulocyte lysate (Amersham, N.90) is diluted with  $^{35}$ S-methionine (Amersham, 1000 Ci/mmol) and poly(A) RNA of Example 5.1. on ice to give final concentrations of lysate 70 %,  $^{35}$ S-methionine 2  $\mu$ Ci/ $\mu$ l, and RNA 4  $\mu$ g/ml. The mixture is incubated at  $30^{\circ}$ C for 1 h. 1  $\mu$ l aliquots are removed at 0 and 60 min respectively, spotted on GF/C filters (Whatman) and used for trichloroacetic acid precipitation according to the Maniatis handbook. For gel electrophoresis 2-4  $\mu$ l lysate mixture are diluted with 20  $\mu$ l Laemmli sample buffer, boiled for 2 min and analyzed on a 10 % acrylamide gel [U.K. Laemmli, Nature 227, 680 (1970)]. The gels are run at 30-40 mA constant current for 3-4 h. After fixation the gels are treated 30 min with a fluorographic solution (ENLIGHTNING $\oplus$ , New England Nuclear), dried and exposed to preflashed Kodak X-5 films overnight at room temperature.

5.3. Preparation of polyclonal antibodies specific for rat GdNPF: Rabbits are immunized by subcutaneous and intramuscular injection of about 50  $\mu$ g of purified rat GdNPF [J. Guenther et al., EMBO J. 4, 1963-1968 (1985)] in complete Freund adjuvant (Sigma). Booster injections with about 50  $\mu$ g of purified rat GdNPF are given in incomplete Freund adjuvant at 4 weeks intervals. Serum is collected 10 days after each booster injection and tested for anti-GdNPF antibodies using the immunodot procedure of R. Hawkes et al. [Anal. Biochem. 119, 142-147 (1982)]. Positive sera are obtained following the second booster injection. The immunoglobulins of positive sera are enriched and purified using standard Protein A-Sepharose $\oplus$  CL-4B (Pharmacia) chromatography according to H. Hjelm et al. [FEBS Letters 28, 73-76 (1972)].

5.4. Immunoprecipitation of rat GdNPF synthesized by in vitro translation: 15  $\mu$ l of the incubated in vitro lysate mixture of Example 5.2. is mixed with 10  $\mu$ g anti-GdNPF antibodies of Example 5.3. In 150  $\mu$ l of immunobuffer containing 1 mM PMSF. The mixture is incubated in a siliconized Eppendorf tube for 17 h at  $4^{\circ}$ C. Protein A-Sepharose $\oplus$  CL-4B (Pharmacia) is freshly prepared by swelling the dry powder 2-3 h in PBS, washing it 3 times in immunobuffer containing 2 mg/ml BSA (Pentax, fraction V) and 2 times in the same buffer without BSA. The sepharose is diluted 1:2 with immunobuffer, 15  $\mu$ l of it added to the Eppendorf tubes containing the lysate mixture and the polyclonal antibodies, and the suspension gently agitated for 60 min at room temperature. The sepharose is washed 3 times with immunobuffer containing 0.5-1 % Tween-20 $\oplus$ . After the final wash 20  $\mu$ l Laemmli sample buffer are pipetted to the dry sepharose pellet. The suspension is incubated 10 min at room temperature and finally boiled for 4 min. After cooling in ice and centrifugation, 20  $\mu$ l of the supernatant are loaded on a 10 % polyacrylamide gel. The gel electrophoresis is run and developed as described above in Example 5.2.

Out of the pools of 48 colonies (Example 5.1), one is positive. The 48 colonies of this one pool are combined to 6 new pools of 8 colonies, and treated alike. Finally, a single colony is identified which gives a positive immunoprecipitation after translation. The clone is expanded in LB-broth containing 20  $\mu$ g/ml tetracycline.

5.5. Sequencing of rat GdNPF cDNA: The cDNA of the positive clone of Example 5.4 is sequenced using the

general method of Sanger. 1.5 µg of the recombinant plasmid derived from pBR322 (Example 4.2) in 9 µl water are mixed with 1 µl (0.5 pmoles) of a primer complementary to the pBR322 derived vector just in front of the Pst 1 endonuclease cleavage site. The DNA is denatured by heating for 3 min in boiling water, frozen for 1 min in dry ice/ethanol, thawed at room temperature and mixed with 1 µl 100 mM Tris-HCl pH 8.3/50 mM MgCl<sub>2</sub>. The annealing mixture is incubated for 30 min at 37°C. The sequencing reaction is performed as described in the Amersham sequencing manual (M 13 cloning and sequencing handbook, Amersham). The sequence found is depicted in formula V.

#### Example 6: Cloning of human GdNPF cDNA

6.1. Human glioma cells: Five human glioma cell lines established by Drs. E.H. Macintyre and N. de Tribolet [J.P. Perkins et al., Life Sciences 10, 1069-1080 (1971), B. de Muret et al., Eur.J.Cancer Clin.Oncol. 21, 207-216 (1985)] are analyzed by Northern blot for the presence of mRNA hybridizing with a DNA probe labelled with <sup>32</sup>P by *in vitro* nick translation of the positive rat GdNPF cDNA clone of Example 5. 10 µg of total cytoplasmic RNA are used per lane. Hybridisation is done for 15 h at 42°C using 1x10<sup>6</sup> cpm of the nick translated probe per ml. The filters are washed four times for 5 min in 30 mM sodium citrate, pH 7.0/300 mM NaCl/0.1 % SDS at room temperature and two times for 15 min in 1.5 mM sodium citrate, pH 7.0/15 mM NaCl/0.1 % SDS at 60°C. Cell line LN-340, which has been deposited at the "Collection Nationale de Cultures de Microorganismes", Institut Pasteur, Paris, on February 5, 1986 under the number I-518, gives strong hybridization and is grown to confluency in 40 10 cm tissue culture dishes.

6.2. Isolation of mRNA: A one ml pellet of human glioma cells LN-340 containing approximately 10<sup>8</sup> cells is dissolved in 6 ml of a filtered solution prepared from 100 g of guanidinium thiocyanate, 100 ml of H<sub>2</sub>O, 10.6 ml 1 M Tris-HCl, pH 7.5, 4.2 ml 0.5 M EDTA, 21.2 ml 20% N-laurylsarcosine and 2.1 ml of 2-mercaptoethanol. After vigorous shaking 2.7 g of baked CsCl are added and the solution is layered over a 2 ml cushion of 5.7 M CsCl in 0.1 M EDTA, pH 7.5 in a 12 ml centrifuge tube. The tube is filled up with H<sub>2</sub>O and centrifuged for 16 h at 29000 rpm at 20°C in a TST 41 rotor (Kontron). At the end of the run most of the supernatant is removed and the tube is drained by quickly inverting. The glazy RNA pellet is dissolved in 0.4 ml of 10 mM Tris-HCl, pH 7.5 and 0.2 % SDS by vortexing and occasional warming (2 min) at 37°C. The RNA is precipitated by addition of 1 ml of ethanol and centrifugation in an Eppendorf centrifuge for 5 min. The RNA (1.1 mg) is air dried and dissolved in 0.5 ml of elution buffer. After heating for 2 min at 68°C and chilling on ice, 55 µl of 5 M NaCl are added and the solution is applied to a 2 ml column of oligo-dT cellulose (type 7, P-L Biochemicals) equilibrated in wash buffer. After three subsequent applications of the sample the column is washed with 15 ml of wash buffer, and the bound RNA eluted with 4 ml of elution buffer. The eluted material is heated for 2 min at 68°C, chilled and 0.44 ml of 5 M NaCl are added. The solution is applied to the re-equilibrated oligo-dT cellulose column (3x). After washing with 15 ml of wash buffer the bound RNA is eluted with 4 ml of elution buffer. The RNA is precipitated overnight at -20°C by addition of 0.25 ml of 3 M NaOAc pH 5.5 and 10 ml of ethanol. The precipitate (76 µg) is collected by centrifugation (15 min at 16000 g), dissolved in 0.4 ml H<sub>2</sub>O and re-precipitated by addition of 25 µl of 3 M NaOAc and 1 ml of ethanol. After chilling in dry-ice for 10 min the RNA is collected by centrifugation for 5 min in an Eppendorf centrifuge. The pellet is air dried and dissolved in 75 µl of H<sub>2</sub>O.

6.3. Preparation of cDNA: 10 µl (1 mg/ml) of the RNA solution is incubated in a solution containing 25 µl RVT buffer, 2.5 µl dNTP mix (20 mM of dATP, dCTP, dTTP, and dGTP each), 5 µl of 1 mg/ml oligo-dT<sub>12-18</sub> (P-L Biochemicals), 1 µl α-<sup>32</sup>P-dCTP (10 µCi, 3000 Ci/mmol), 3 µl RNasin® (60 units, Biotec), 3 µl reverse transcriptase (66 units, Genofit), and 2 µl of H<sub>2</sub>O. The mixture is incubated for 1.5 h at 42°C, then the reaction stopped by addition of 2 µl 0.5 M EDTA, pH 7.5. The RNA is degraded by addition of 25 µl 0.15 M NaOH and incubation at 65°C for 1 h. The solution is neutralized by addition of 25 µl of 1 M Tris-HCl, pH 8.0 and 6 µl of 1 M HCl. 2 µl of 20 % SDS are added and the solution is extracted with 0.15 ml phenol-chloroform mix (equal volumes of phenol and chloroform, 0.1 % δ-hydroxyquinoline and equilibrated with 10 mM Tris-HCl, pH 8.0, 1 mM EDTA and 0.1 M NaCl). The aqueous phase is applied to a 2 ml Sephadex® G-50 (medium) column in a pasteur pipet equilibrated with TNE buffer. The breakthrough fraction (0.4 ml) containing 3 µg of cDNA is collected, and the cDNA precipitated by addition of 1 ml ethanol and chilling in dry-ice for 10 min. After centrifugation (5 min, Eppendorf centrifuge) the air-dried pellet is dissolved in 32 µl H<sub>2</sub>O. The cDNA is extended with oligo-dC tails in a reaction mixture containing 32 µl cDNA (2.8 µg), 10 µl 1 M potassium cacodylate, pH 7.0, 5 µl 10 mM CoCl<sub>2</sub>, 5 µl 1 mM DTT and 10 µCi of <sup>3</sup>H-dCTP (20 Ci/mmol, 10 µl lyophilized). After preincubation for 5 min at 37°C 3 µl of terminal deoxynucleotidyl transferase (81 units, P-L Biochemicals) are added and incubation is allowed to proceed for 10 min. 50 µl of TNE buffer are added and the solution is extracted with 0.1 ml phenol-chloroform mix. The cDNA is precipitated by addition of 0.1 ml ethanol and chilling in dry-ice. After centrifugation the pellet is washed with 70 % ethanol, air-dried and dissolved in 13 µl of H<sub>2</sub>O.

6.4. Preparation of ds cDNA: Above solution of cDNA in 13 µl H<sub>2</sub>O, 25 µl RVT buffer, 2.5 µl dNTP mix (20 mM of dATP, dCTP, dTTP and dGTP each), 5 µl 0.2 mg/ml oligo-dG<sub>12-18</sub> (P-L Biochemicals), 3 µl α-<sup>32</sup>P-dCTP (10 µCi/ml, 3000 Ci/mmol) and 3 µl of reverse transcriptase (66 units, Genofit) are incubated at 42°C for 1.5 h. The reaction is stopped by addition of 2 µl 0.5 M EDTA, pH 7.5 and 50 µl TNE buffer, and the mixture is extracted with 0.15 ml phenol-chloroform mix. The aqueous phase is applied onto a Sephadex® G-50 column (2.5 ml in TNE buffer) and the breakthrough fraction (0.4 ml) containing 1.8 µg of ds cDNA is collected. The DNA is precipitated by addition of 1 ml ethanol and chilling in dry-ice. The resulting pellet is taken up in 32 µl H<sub>2</sub>O and the DNA extended with oligo-dC tails as described in Example 6.3 for single-stranded cDNA. The reaction is stopped by addition of 1 µl 0.5 M EDTA, pH 7.5, and the sample loaded onto a horizontal 1 %

agarose gel in TBE buffer using slots with a width of 0.5 cm. After electrophoresis for 1 h at 5 V/cm, the region containing cDNA with an approximate size between 1.5 and 2 kilobases is excised and placed in two micro-collodion bags (Sartorius) and presoaked in H<sub>2</sub>O. 0.3 ml H<sub>2</sub>O are added and the bags are placed in an electrophoresis apparatus containing half-concentrated TBE buffer. The DNA is electroeluted at 5 V/cm electrode distance for 20 min and recovered from the bag by vigorous pipetting. After extraction with 0.6 ml phenol-chloroform mix, 40 µl of 3 M NaOAc pH 5.5 and 1.2 ml ethanol are added and the solution chilled in dry-ice for 10 min. After centrifugation (5 min, Eppendorf-centrifuge) 90 ng of ds cDNA are recovered and dissolved in 20 µl of 10 mM Tris-HCl, pH 8.0 and 1 mM EDTA.

6.5. Annealing of cut pUC9 with poly(dG) tails to ds cDNA with poly(dC) tails and transformation of *E. coli* with the obtained plasmid: 20 µl cDNA (90 ng of size-fractionated material of Example 6.4) is mixed with 8 µl (100 ng) of oligo-dG<sub>10-20</sub> tailed pUC9 DNA (Pharmacia) and 172 µl TNE buffer and sequentially incubated at 65°C for 10 min, at 46°C for 1 h, at 37°C for 1 h and at room temperature for 1 h. The annealed cDNA-plasmid DNA is used to transform competent *E. coli* HB 101 cells (strain LM 1035), which have been prepared for transformation as described in the Maniatis handbook. 1 µl of annealed DNA is added to 200 µl of competent cells and left on ice for 30 min. This procedure is performed 60 times. After heat shock of 90 sec and chilling in ice for 2 min, 0.8 ml of SOC medium is added per tube which is then incubated for 60 min at 37°C. SOC medium contains 2 % Bacto trypton, 0.5 % yeast extract (both from Gibco), 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl<sub>2</sub>, 5 mM MgSO<sub>4</sub> and 20 mM glucose. After the incubation all tubes are combined and plated out on 3 McConkey agar plates (15 cm) containing 50 µg/ml of ampicillin. The plates are incubated overnight at 37°C. The resulting 2500 recombinants per plate are lifted onto nylon membranes (Pall-Biodyne) and two replicas made. The master filter is stored at 4°C on an agar plate and the replicas are processed for colony hybridization as described in the Maniatis handbook.

#### Example 7: Hybridization of human cDNA derived from glioma cell with cDNA coding for rat GdNPF

The cDNA insert from 1 µg plasmid coding for rat GdNPF obtained from the positive clone of Example 5 is removed by digestion with Pst I restriction endonuclease, agarose gel electrophoresis and gel elution. The pure cDNA insert (100 ng) is rendered radioactive using a nick translation kit from Amersham (N.5000) following the instructions given by the supplier. The radioactive cDNA probe has a specific activity of  $5 \times 10^8$  dpm/µg.

The replica filters (Example 6.5) are prehybridized for 2 h in 100 ml of a solution containing 0.9 M NaCl, 0.18 M Tris-HCl, pH 8.0, 6 mM EDTA, 0.02 % Ficoll 400, 0.02 % polyvinylpyrrolidone, 0.02 % BSA, 0.2 % SDS and 50 µg/ml of denatured calf thymus DNA. Hybridization is performed over night in 1 ml of the same solution containing the heat-denatured nick-translated cDNA probe ( $60 \times 10^6$  dpm) in a sealed plastic bag. After hybridization the filters are washed in 200 ml of 0.9 M NaCl, 0.18 M Tris-HCl, pH 8.0, 6 mM EDTA and 0.2 % SDS, twice at 65°C, followed by two washes at 65°C with 200 ml of 0.45 M NaCl, 0.09 M Tris-HCl, pH 8.0, 3 mM EDTA and 0.2 % SDS and two washes with 200 ml of 0.15 M NaCl, 0.03 M Tris-HCl, pH 8.0, 1 mM EDTA and 0.2 % SDS. The filters are exposed on an X-ray film over night and positives appear on both replica filters. The eleven positive colonies are grown up and their plasmid DNAs are isolated for restriction analysis. Two recombinant plasmids containing inserts of approximately  $1.5 \times 10^3$  nucleotides are chosen for restriction analysis as described in the Maniatis handbook and for determination of the full coding sequences using the method of Sanger (M13 cloning and sequencing handbook, Amersham). A summary of the restriction and sequence analysis is given in the drawing. The full sequence is depicted in formula IV. One clone gives a DNA of the formula IV, wherein W is A (hence X<sub>2</sub> is Arg), and the other clone gives a DNA sequence of the formula IV, wherein W is ACAG (hence X<sub>2</sub> is Thr-Gly).

#### Example 8: Synthesis of human GdNPF by *E. coli* containing plasmids coding for human GdNPF

One of the two clones of Example 7 shown to contain the DNA sequence of formula IV is grown in tryptone medium to an optical density (OD<sub>650</sub>) of about 1. The cells are harvested and resuspended in 0.5 ml of an aqueous solution containing 30 mM NaCl and 50 mM Tris-HCl, pH 8.0. Lysozyme (Sigma) is added to 1 mg/ml. After 30 min. at 0°C, the suspensions are frozen in liquid nitrogen and thawed at 37°C five times, then centrifuged for 20 min at 20 000 rpm in an SS 34 Sorvall rotor at 4°C. The supernatants are tested using the casein degradation assay of Example 2 and the neurite outgrowth assay of Example 9. The human GdNPF is purified by chromatography on heparin-Sepharose® CL-6B followed by chromatography on Affi-Gel Blue® as described for rat GdNPF by Guenther et al [EMBO J. 4, 1963-1966 (1985)].

#### Example 9: Neurite outgrowth assay

Culture dishes (35 mm) are inoculated with 40 000 EDTA-dislodged mouse neuroblastoma cells, clone NB2A (ATCC Cell Depository Number CCL 131), and incubated in DMEM containing 10 % FCS at 37°C in a humidified atmosphere containing 10 % CO<sub>2</sub>. After 16-18 h the medium is replaced by DMEM containing 0.5 % FCS dialyzed exhaustively against 0.9 % NaCl solution (but not heat inactivated), then filter-sterilized and frozen. After 22 h 100 µl of a cell supernatant of Example 8 in a final volume of 2.0 ml DMEM is added. The assay is terminated after 4 h by fixation of the cells with 2.5 % glutaraldehyde in PBS. The extent of morphological differentiation is determined by phase contrast microscopy as described by D. Monard et al. [Proc. Nat. Acad. Sci. USA 70, 1894-1897 (1973)].

**Example 10: Demonstration of relationship between novel human GdNPF and known rat GdNPF**

About 250 µg of rat GdNPF [J. Guenther et al., EMBO J. 4, 1963-1966 (1985)] is reduced and carboxymethylated according to V.T. Ruegg et al. [Methods in Enzymology 47, 111-116 (1977)]. The reaction mixture is dialyzed against 0.1 % TFA, concentrated to 1 ml with a Savant Speed Vac concentrator and desalted by reversed phase high pressure liquid chromatography. The sample is injected on a widepore C<sub>8</sub>-RP column 0.4 x 25 cm (Bakerbond® RP 7105-0, J.T. Baker) and processed with 0.1 % TFA in a gradient of 40 % to 50 % aqueous acetonitrile in 30 min. The fraction containing the protein is freed from acetonitrile and concentrated to 0.5 ml (Savant Speed Vac concentrator). The resulting solution, 120 µl of 1 M NH<sub>4</sub>HCO<sub>3</sub> and 2 µg trypsin (Worthington) in 10 µl 10<sup>-3</sup> M HCl are incubated for 24 h at 37° C. The reaction mixture is acidified to pH 2 with TFA and purified by high pressure liquid chromatography on the same column as above. The sample is processed with 0.1 % aqueous TFA (5 min), then a gradient of 0.1 % TFA in 0 % to 50 % aqueous acetonitrile in 90 min. Fractions containing five different polypeptides clearly separated during the first half of the chromatography are collected and concentrated to 20 µl, then sequenced on a commercial gas-liquid phase sequencer (Applied Biosystems).

The following sequences are found:

- 1) Thr-Phe-Val-Ala-Gly-Asp-Gly-Lys, related to sequence 187 to 194 of human GdNPF, wherein Ala replaces <sup>5</sup>Gly
- 2) Phe-Gln-Pro-Glu-Asn-Thr-Lys, identical with sequence 178 to 184 of human GdNPF,
- 3) Thr-Ile-Asn-Ser-Trp or Thr-Met-Asn-Thr-Met-Val-Pro-Lys, related to sequence 257 to 268 of human GdNPF,
- 4) Ala-Ile-Val-Ser-Lys, identical with sequence 79 to 83 of human GdNPF, and
- 5) Ala-Asn-Phe-Ala-Lys, identical with sequence 303 to 307 of human GdNPF.

These results indicate that the isolated human cDNA indeed corresponds to the coding sequence of GdNPF and does not represent an artefact.

**Example 11: Synthesis of GdNPF fragments**

The peptides are synthesized using the solid-phase method developed by Merrifield [A. Marglin & R.B. Merrifield, Ann. Rev. Biochem. 39, 841-866 (1970)] with two minor modifications: The tert-butoxycarbonyl-protected amino acids are activated for condensation by the addition of dicyclohexylcarbodiimide and 1-hydroxybenzotriazole [W. König & R. Geiger, Chem. Ber. 103, 788-798 (1979)], and the resin is washed alternately with solvents that favour swelling and extreme shrinking [L. Corley, D.M. Sachs & C.B. Anfinsen, Biochem., Biophys. Res. Commun. 47, 1353-1359 (1972)].

11.1. Peptide synthesis protocol: The C-terminal amino acid is condensed with chloromethylated polystyrene resin (Merrifield polymer, FLUKA, Buchs, Switzerland) according to the procedure of B.F. Gisin [Helv. Chim. Acta 56, 1476-1482 (1973)]. The peptide synthesis is carried out manually in a reactor designed by M.A. Juillerat (Nestec SA, Switzerland). Mixing is achieved by flushing nitrogen through the reactor vessel.

A reaction cycle consists of:

- (a) 50 % TFA/CH<sub>2</sub>Cl<sub>2</sub>, 5 min
- (b) 50 % TFA/CH<sub>2</sub>Cl<sub>2</sub>, 25 min
- (c) CH<sub>2</sub>Cl<sub>2</sub>, three times 2 min
- (d) CHCl<sub>3</sub>, three times 2 min
- (e) triethylamine/CHCl<sub>3</sub> 1:9, twice 5 min
- (f) CHCl<sub>3</sub>, three times 2 min
- (g) dimethylformamide (DMF), three times 2 min
- (h) 4 equivalents tert-butoxycarbonyl-protected amino acid and 4 equivalents 1-hydroxybenzotriazole in DMF, followed after 1 min by 4 equivalents dicyclohexylcarbodiimide in CH<sub>2</sub>Cl<sub>2</sub>, 60 min
- (i) DMF, twice 2 min
- (j) CH<sub>2</sub>Cl<sub>2</sub>, twice 2 min
- (k) CH<sub>3</sub>OH, twice 5 min
- (l) CH<sub>2</sub>Cl<sub>2</sub>, three times 2 min
- (m) second coupling with 2.5 equivalents of the same protected amino acid, steps (d)-(l)
- (n) 1 % N-acetylimidazole and 10 % acetic anhydride in CH<sub>2</sub>Cl<sub>2</sub>, 30 min.

The following N<sup>α</sup>-tert-butoxycarbonyl(N-BOC)-L-amino acids (Bachem Fine Chemicals, Bubendorf, Switzerland) are used:

- N<sup>α</sup>-BOC-L-alanine
- N<sup>α</sup>-BOC-N<sup>α</sup>-nitro-L-arginine
- N-BOC-L-aspartic acid-β-cyclohexylester
- N-BOC-L-glutamine
- N-BOC-L-glutamic acid-γ-benzylester
- N-BOC-L-glycine
- N<sup>α</sup>-BOC-N<sup>α</sup>-tosyl-L-histidine
- N-BOC-L-isoleucine
- N<sup>α</sup>-BOC-N<sup>α</sup>-2-chlorobenzoyloxycarbonyl-L-lysine
- N-BOC-L-phenylalanine
- N-BOC-L-proline

N-BOC-O-benzyl-L-serine  
 N-BOC-O-benzyl-L-threonine  
 N-BOC-L-tryptophane  
 N-BOC-L-valine

A larger excess of 6 to 8 equivalents is used in the coupling of steps (h) and (m) with the tert-butoxycarbonyl-protected amino acids asparagine, glutamine, isoleucine, proline, and threonine. In the cycles following addition of a tryptophane residue, 2 % 1,2-ethanedithiol (Fluka) is added to the deprotection steps (a) and (b) in order to prevent the oxidation of the indole ring. Dehydration of the carboxamide function of glutamine is minimized by performing the 1-hydroxybenzotriazole ester (0°, 15 min) before addition to the resin in step (h).

11.2. Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala: The reactor vessel is charged with 3.55 g (1.92 mmol) of alanyl-substituted resin (0.54 mmol/g resin), and 13 cycles with the corresponding amino acids are run. The peptide synthesis is monitored by ninhydrin analysis of small aliquots. The final peptide-resin is treated with 35 ml of hydrogen fluoride/anisole (10:1, v/v) for 1 hour at 0°C. The hydrogen fluoride is removed at 0°C under reduced pressure. The resin is washed three times with ethyl acetate, then extracted with three portions of 50 ml 50 % acetic acid. The extracts are lyophilized, and the residue purified by high pressure liquid chromatography using a Whatman preparative column Partisil® 10 ODS-3, 25 cm, using 0.1 % TFA (10 min), then 0.1 % TFA in a gradient of 0 to 50 % acetonitrile (60 min). The pure product is characterized by amino acid sequencing on a commercial gas-liquid phase sequencer (Applied Biosystems).

11.3. His-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala: This protein is prepared in a manner completely analogous to Example 11.2 except for substituting histidine for glutamine in the last cycle.

11.4. Arg-Ser-Ser-Pro-Trp-Phe-Ile-Val-Asp-Ser-Phe: The reactor vessel is charged with 3.0 g (1.29 mmol) of phenylalanyl-substituted resin (0.43 mmol/g resin), and 11 cycles with the corresponding amino acids are run. Cleavage, deprotection and purification of the product is performed as described in Example 11.2 except that the hydrogen fluoride/anisole mixture additionally contains 2 % 1,2-ethanedithiol.

11.5. Lys-Ser-Arg-Phe-Gln-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe: This protein is prepared in a manner analogous to Example 11.4 in 13 cycles with the corresponding amino acids.

#### Example 12: Pharmaceutical preparation for parenteral application

200 µg of human GdNPF are dissolved in 3 ml of 5N human serum albumin. The resulting solution is passed through a bacteriological filter and the filtered solution subdivided under aseptic conditions into 10 vials. The vials are preferably stored in the cold, for example at -20°C.

#### Claims

1. Essentially pure human glia-derived neurite-promoting factor (GdNPF), related polypeptides and fragments thereof retaining neurite-promoting activity.

2. Human GdNPF according to claim 1 of the formula

X<sub>1</sub>-Ser-His-Phe-Asn-Pro-Leu-Ser-Leu-Glu-Glu-Gly-Ser-Asn-Thr-Gly- 16  
 Ile-Gln-Val-Phe-Asn-Gln-Ile-Val-Lys-Ser-Arg-Pro-His-Asp-Asn-Ile- 32  
 Val-Ile-Ser-Pro-His-Gly-Ile-Ala-Ser-Val-Leu-Gly-Met-Leu-Gln-Leu- 48  
 Gly-Ala-Asp-Gly-Arg-Thr-Lys-Lys-Gln-Leu-Ala-Met-Val-Met-Arg-Tyr- 64  
 Gly-Val-Asn-Gly-Val-Gly-Lys-Ile-Leu-Lys-Lys-Ile-Asn-Lys-Ala-Ile- 80  
 Val-Ser-Lys-Lys-Asn-Lys-Asp-Ile-Val-Thr-Val-Ala-Asn-Ala-Val-Phe- 96  
 Val-Lys-Asn-Ala-Ser-Glu-Ile-Glu-Val-Pro-Phe-Val-Thr-Arg-Asn-Lys- 112  
 Asp-Val-Phe-Gln-Cys-Glu-Val-Arg-Asn-Val-Asn-Phe-Glu-Asp-Pro-Ala- 128  
 Ser-Ala-Cys-Asp-Ser-Ile-Asn-Ala-Trp-Val-Lys-Asn-Glu-Thr-Arg-Asp- 144  
 Met-Ile-Asp-Asn-Leu-Leu-Ser-Pro-Asp-Leu-Ile-Asp-Gly-Val-Leu-Thr- 160  
 Arg-Leu-Val-Leu-Val-Asn-Ala-Val-Tyr-Phe-Lys-Gly-Leu-Trp-Lys-Ser- 176  
 Arg-Phe-Gln-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe-Val-Ala-Ala-Asp- 192  
 Gly-Lys-Ser-Tyr-Gln-Val-Pro-Met-Leu-Ala-Gln-Leu-Ser-Val-Phe-Arg- 208  
 Cys-Gly-Ser-Thr-Ser-Ala-Pro-Asn-Asp-Leu-Trp-Tyr-Asn-Phe-Ile-Glu- 224  
 Leu-Pro-Tyr-His-Gly-Glu-Ser-Ile-Ser-Met-Leu-Ile-Ala-Leu-Pro-Thr- 240  
 Glu-Ser-Ser-Thr-Pro-Leu-Ser-Ala-Ile-Ile-Pro-His-Ile-Ser-Thr-Lys- 256  
 Thr-Ile-Asp-Ser-Trp-Met-Ser-Ile-Met-Val-Pro-Lys-Arg-Val-Gln-Val- 272  
 Ile-Leu-Pro-Lys-Phe-Thr-Ala-Val-Ala-Gln-Thr-Asp-Leu-Lys-Glu-Pro- 288  
 Leu-Lys-Val-Leu-Gly-Ile-Thr-Asp-Met-Phe-Asp-Ser-Ser-Lys-Ala-Asn- 304  
 Phe-Ala-Lys-Ile-Thr-X<sub>2</sub>-Ser-Glu-Asn-Leu-His-Val-Ser-His-Ile-Leu- 320  
 Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala-Ser-Ala- 336  
 Ala-Thr-Thr-Ala-Ile-Leu-Ile-Ala-Arg-Ser-Ser-Pro-Pro-Trp-Phe-Ile- 352  
 Val-Asp-Arg-Pro-Phe-Leu-Phe-Phe-Ile-Arg-His-Asn-Pro-Thr-Gly-Ala- 368  
 Val-Leu-Phe-Met-Gly-Gln-Ile-Asn-Lys-Pro 378  
 (I),

optionally glycosylated, wherein Cys is optionally in the disulfide form, X<sub>1</sub> is hydrogen, acyl, the peptide residue of the formula

Met-Asn-Trp-His-Leu-Pro-Leu-Phe-Leu-Leu-Ala-Ser-Val-Thr-Leu-Pro-Ser-

-1  
Ile-Cys- (II)

or a fragment of the residue of formula II comprising between 1 and 18 amino acids from the carboxyl end, optionally in acylated form, and X<sub>2</sub> is Arg or Thr-Gly, related polypeptides retaining neurite-promoting activity, wherein one or more single amino acids in the compound of the formula I are replaced by other amino acids, and fragments of the compound of the formula I comprising at least 10 consecutive amino acids selected from the amino acid chain between the amino acid 29 and amino acid 378 and optionally one or more other amino acids.

3. Human GDNF according to claim 2 of the formula I, wherein Cys is optionally in the disulfide form and X<sub>1</sub> is hydrogen, acetyl, the peptide residue of the formula II or a fragment of the residue of formula II comprising between 1 and 18 amino acids from the carboxyl end.

4. Human GdNPF according to claim 2 or 3 of the formula I, wherein Cys is optionally in the disulfide form and X<sub>1</sub> is hydrogen, the peptide residue of the formula II, the fragment comprising the amino acids -18 to -1 of the formula II, Pro-Ser-Ile-Cys-, Ser-Ile-Cys-, Ile-Cys-, or Cys-.

5. Human GdNPF according to claim 2, 3 or 4 wherein X<sub>2</sub> is Arg.

6. Human GdNPF according to claim 2, 3 or 4 wherein X<sub>2</sub> is Thr-Gly.

7. A GdNPF-related polypeptide according to claim 1 of formula 1, wherein X<sub>1</sub> and X<sub>2</sub> have the meaning given in claim 2 and wherein one, two, three or four single amino acids are replaced by other amino acids.

8. A fragment according to claim 1 comprising at least 10 consecutive amino acids of the compound of the formula I, wherein X<sub>2</sub> is Arg or Thr-Gly, selected from the amino acid chain between the amino acid 29 and amino acid 378, and optionally one or more other amino acids.

9. A fragment according to claim 8 comprising amino acids 2 to 378, 3 to 378, 4 to 378, 5 to 378 6 to 378 or 7 to 378 of the compound of the formula I.

10. A fragment according to claim 8 comprising 10 to 50 consecutive amino acids of formula I including <sup>310</sup>Arg and <sup>311</sup>Ser and/or <sup>345</sup>Arg and <sup>346</sup>Ser and optionally one, two or three other amino acids.

11. A fragment according to claim 8 comprising 10 to 50 consecutive amino acids of formula I including amino acids selected from the amino acid chain 72 to 96, 134 to 146, 159 to 195 or 314 to 378, and optionally one, two or three other amino acids.

12. A fragment according to claim 8 or 11 of the formula Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala.

13. A fragment according to claim 8 or 11 of the formula His-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala.

14. A fragment according to claim 8 or 11 of the formula Arg-Ser-Ser-Pro-Pro-Trp-Phe-Ile-Val-Asp-Ser-Phe.

15. A fragment according to claim 8 or 11 of the formula Lys-Ser-Arg-Phe-Gln-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe.

16. A process for the preparation of human GdNPF, related peptides and fragments thereof retaining neurite-promoting activity comprising isolating the desired compound from cells producing it or synthesizing it by condensation reactions.

17. A process according to claim 16, comprising the steps of

a) isolating a DNA coding for GdNPF or a fragment thereof from a cDNA library of glial cells or a genomic DNA library and optionally mutating it, or chemically synthesizing such a DNA.

b) incorporating the DNA into an appropriate expression vector,

c) transferring the obtained hybrid vector into a recipient host,

d) selecting the transformed host from untransformed hosts by culturing under conditions under which only the transformed host survives.

e) culturing the transformed host under conditions which allow expression of the heterologous polypeptide, and

f) isolating the human GdNPF, related peptide, or fragment thereof.

18. A process according to claim 16, characterized in that a N-protected amino acid is coupled to a suitable resin, the protecting group is removed, a second N-protected amino acid is condensed with the amino group of the first amino acid, the cycle of deprotection/condensation with the next N-protected amino acid is repeated until the peptide residue of the desired composition is complete, and finally this peptide residue is cleaved from the resin and deprotected.

19. A DNA coding for GdNPF, a mutant thereof, a DNA coding for related polypeptides retaining neurite-promoting activity or a fragment of such DNA comprising at least 15 nucleotides.

20. A DNA according to claim 19 of the formula

Z<sub>1</sub>-Y<sub>13</sub>-Y<sub>3</sub>-Y<sub>18</sub>-Y<sub>9</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>14</sub>-Y<sub>11</sub>-Y<sub>11</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>20</sub>-Y<sub>17</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>18</sub>-Y<sub>10</sub>-Y<sub>5</sub>-Y<sub>16</sub>-Y<sub>9</sub>-Y<sub>14</sub>-Y<sub>3</sub>-  
 Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>18</sub>-Y<sub>11</sub>-Y<sub>7</sub>-Y<sub>7</sub>-Y<sub>11</sub>-Y<sub>6</sub>-Y<sub>16</sub>-Y<sub>3</sub>-Y<sub>17</sub>-Y<sub>8</sub>-Y<sub>10</sub>-Y<sub>6</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>3</sub>-Y<sub>6</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>12</sub>-Y<sub>16</sub>-Y<sub>2</sub>-Y<sub>15</sub>-Y<sub>9</sub>-Y<sub>4</sub>-  
 Y<sub>3</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>10</sub>-Y<sub>16</sub>-Y<sub>15</sub>-Y<sub>9</sub>-Y<sub>8</sub>-Y<sub>10</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>13</sub>-Y<sub>11</sub>-Y<sub>6</sub>-Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>1</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>2</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>12</sub>-Y<sub>8</sub>-  
 Y<sub>11</sub>-Y<sub>1</sub>-Y<sub>13</sub>-Y<sub>20</sub>-Y<sub>13</sub>-Y<sub>2</sub>-Y<sub>19</sub>-Y<sub>8</sub>-Y<sub>20</sub>-Y<sub>3</sub>-Y<sub>8</sub>-Y<sub>20</sub>-Y<sub>8</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>12</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>16</sub>-Y<sub>12</sub>-  
 Y<sub>12</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>4</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>17</sub>-Y<sub>20</sub>-Y<sub>1</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>20</sub>-Y<sub>12</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>7</sub>-Y<sub>10</sub>-Y<sub>7</sub>-Y<sub>20</sub>-Y<sub>16</sub>-Y<sub>14</sub>-Y<sub>20</sub>-Y<sub>17</sub>-  
 Y<sub>2</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>4</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>6</sub>-Y<sub>5</sub>-Y<sub>7</sub>-Y<sub>20</sub>-Y<sub>2</sub>-Y<sub>3</sub>-Y<sub>20</sub>-Y<sub>3</sub>-Y<sub>14</sub>-Y<sub>7</sub>-Y<sub>4</sub>-Y<sub>15</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>5</sub>-Y<sub>4</sub>-Y<sub>16</sub>-Y<sub>10</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>18</sub>-  
 Y<sub>20</sub>-Y<sub>12</sub>-Y<sub>3</sub>-Y<sub>7</sub>-Y<sub>17</sub>-Y<sub>2</sub>-Y<sub>4</sub>-Y<sub>13</sub>-Y<sub>10</sub>-Y<sub>4</sub>-Y<sub>3</sub>-Y<sub>11</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>15</sub>-Y<sub>4</sub>-Y<sub>11</sub>-Y<sub>10</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>17</sub>-Y<sub>2</sub>-Y<sub>11</sub>-Y<sub>20</sub>-  
 Y<sub>11</sub>-Y<sub>20</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>19</sub>-Y<sub>14</sub>-Y<sub>12</sub>-Y<sub>8</sub>-Y<sub>11</sub>-Y<sub>18</sub>-Y<sub>12</sub>-Y<sub>16</sub>-Y<sub>2</sub>-Y<sub>14</sub>-Y<sub>6</sub>-Y<sub>15</sub>-Y<sub>7</sub>-Y<sub>3</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>12</sub>-Y<sub>2</sub>-Y<sub>17</sub>-Y<sub>17</sub>-Y<sub>14</sub>-Y<sub>20</sub>-  
 Y<sub>1</sub>-Y<sub>1</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>12</sub>-Y<sub>16</sub>-Y<sub>18</sub>-Y<sub>6</sub>-Y<sub>20</sub>-Y<sub>15</sub>-Y<sub>13</sub>-Y<sub>11</sub>-Y<sub>1</sub>-Y<sub>6</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>2</sub>-Y<sub>6</sub>-Y<sub>8</sub>-Y<sub>16</sub>-Y<sub>17</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>15</sub>-  
 Y<sub>3</sub>-Y<sub>4</sub>-Y<sub>11</sub>-Y<sub>18</sub>-Y<sub>19</sub>-Y<sub>3</sub>-Y<sub>14</sub>-Y<sub>10</sub>-Y<sub>7</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>19</sub>-Y<sub>8</sub>-Y<sub>8</sub>-Y<sub>7</sub>-Y<sub>18</sub>-Y<sub>10</sub>-Y<sub>18</sub>-Y<sub>13</sub>-Y<sub>11</sub>-Y<sub>10</sub>-Y<sub>1</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>17</sub>-Y<sub>7</sub>-  
 Y<sub>16</sub>-Y<sub>16</sub>-Y<sub>17</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>10</sub>-Y<sub>10</sub>-Y<sub>15</sub>-Y<sub>9</sub>-Y<sub>10</sub>-Y<sub>16</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>17</sub>-Y<sub>10</sub>-Y<sub>4</sub>-Y<sub>16</sub>-Y<sub>18</sub>-Y<sub>13</sub>-Y<sub>16</sub>-Y<sub>10</sub>-Y<sub>13</sub>-  
 Y<sub>20</sub>-Y<sub>15</sub>-Y<sub>12</sub>-Y<sub>2</sub>-Y<sub>20</sub>-Y<sub>6</sub>-Y<sub>20</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>12</sub>-Y<sub>14</sub>-Y<sub>17</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>1</sub>-Y<sub>6</sub>-Y<sub>17</sub>-Y<sub>4</sub>-Y<sub>11</sub>-Y<sub>12</sub>-Y<sub>7</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>12</sub>-Y<sub>20</sub>-  
 Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>10</sub>-Y<sub>17</sub>-Y<sub>4</sub>-Y<sub>13</sub>-Y<sub>14</sub>-Y<sub>4</sub>-Y<sub>16</sub>-Y<sub>18</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>3</sub>-Y<sub>14</sub>-Y<sub>1</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>17</sub>-Y<sub>22</sub>-Y<sub>16</sub>-Y<sub>7</sub>-Y<sub>3</sub>-Y<sub>11</sub>-Y<sub>9</sub>-Y<sub>20</sub>-  
 Y<sub>18</sub>-Y<sub>9</sub>-Y<sub>10</sub>-Y<sub>1</sub>-Y<sub>6</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>7</sub>-Y<sub>20</sub>-Y<sub>16</sub>-Y<sub>7</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>1</sub>-Y<sub>17</sub>-Y<sub>17</sub>-Y<sub>1</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>10</sub>-  
 Y<sub>1</sub>-Y<sub>2</sub>-Y<sub>16</sub>-Y<sub>18</sub>-Y<sub>15</sub>-Y<sub>15</sub>-Y<sub>18</sub>-Y<sub>14</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>4</sub>-Y<sub>2</sub>-Y<sub>16</sub>-Y<sub>14</sub>-Y<sub>11</sub>-Y<sub>14</sub>-Y<sub>14</sub>-Y<sub>10</sub>-Y<sub>2</sub>-Y<sub>9</sub>-Y<sub>3</sub>-Y<sub>15</sub>-Y<sub>17</sub>-Y<sub>8</sub>-Y<sub>1</sub>-Y<sub>20</sub>-  
 Y<sub>11</sub>-Y<sub>1</sub>-Y<sub>14</sub>-Y<sub>13</sub>-Y<sub>8</sub>-Y<sub>6</sub>-Y<sub>10</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>15</sub>-Y<sub>21</sub>-Z<sub>2</sub>

(III),

wherein

Y<sub>1</sub> codes for alanine (Ala) and is GCT, GCC, GCA or GCG,  
 Y<sub>2</sub> codes for arginine (Arg) and is CGT, CGC, CGA, CGG, AGA or AGG,  
 Y<sub>3</sub> codes for asparagine (Asn) and is AAT or AAC,  
 Y<sub>4</sub> codes for aspartic acid (Asp) and is GAT or GAC,  
 Y<sub>6</sub> codes for cysteine (Cys) and is TGT or TGC,  
 Y<sub>8</sub> codes for glutamine (Gln) and is CAA or CAG,  
 Y<sub>7</sub> codes for glutamic acid (Glu) and is GAA or GAG,  
 Y<sub>8</sub> codes for glycine (Gly) and is GGT, GGC, GGA or GGG,  
 Y<sub>9</sub> codes for histidine (His) and is CAT or CAC,  
 Y<sub>10</sub> codes for isoleucine (Ile) and is ATT, ATC or ATA,  
 Y<sub>11</sub> codes for leucine (Leu) and is TTA, TTG, CTT, CTC, CTA or CTG,  
 Y<sub>12</sub> codes for lysine (Lys) and is AAA or AAG,  
 Y<sub>13</sub> codes for methionine (Met) and is ATG,  
 Y<sub>14</sub> codes for phenylalanine (Phe) and is TTT or TTC,  
 Y<sub>15</sub> codes for proline (Pro) and is CCT, CCC, CCA or CCG,  
 Y<sub>16</sub> codes for serine (Ser) and is TCT, TCC, TCA, TCG, AGT or AGC,  
 Y<sub>17</sub> codes for threonine (Thr) and is ACT, ACC, ACA or ACG,  
 Y<sub>18</sub> codes for tryptophan (Trp) and is TGG,  
 Y<sub>19</sub> codes for tyrosine (Tyr) and is TAT or TAC,  
 Y<sub>20</sub> codes for valine (Val) and is GTT, GTC, GTA or GTG,  
 Y<sub>21</sub> is a stop codon TAA, TAG or TGA,  
 Y<sub>22</sub> is Y<sub>2</sub> or Y<sub>17</sub>-Y<sub>8</sub>,  
 Z<sub>1</sub> is a flanking DNA residue of 12 nucleotides or more containing a promoter sequence,  
 Z<sub>2</sub> is absent or a flanking DNA residue of one or more nucleotides, and Z<sub>1</sub> and Z<sub>2</sub> are optionally linked,  
 a double-stranded DNA consisting of a DNA of formula III and of a complementary DNA thereto, that  
 complementary DNA itself, a mutant thereof, wherein one or more nucleotides are mutated, and  
 fragments of such DNA comprising at least 15 nucleotides.  
 21. A DNA according to claim 19 or 20 of the formula

MetAsnTrpHisLeuProLeuPheLeuLeuAlaSer -8  
 Z<sub>3</sub>-CGGTCGTCCTTGGTGAAGTAACCACTGAAGTGGCATCTCCCCCTCTTCCTCTTGGCCTCT 60 50  
 -1 1  
 ValThrLeuProSerIleCysSerHisPheAsnProLeuSerLeuGluGluLeuGlySerAsn 14  
 GTGACGCTGCCTTCCATCTGCTCCCACTTCAATCCTCTGTCTCTCGAGGAAGTGGCTCCAAC 123 55  
 ThrGlyIleGlnValPheAsnGlnIleValLysSerArgProHisAspAsnIleValIleSer 35  
 ACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCCTCATGACAACATCGTGATCTCT 186 60  
 65

ProHisGlyIleAlaSerValLeuGlyMetLeuGlnLeuGlyAlaAspGlyArgThrLysLys 56  
 CCCCATGGGATTGCGTCGGTCCTGGGGATGCTTCAGCTGGGGGCGGACGGCAGGACCAAGAAG 249  
  
 GlnLeuAlaMetValMetArgTyrGlyValAsnGlyValGlyLysIleLeuLysLysIleAsn 77  
 CAGCTCGCCATGGTGATGAGATACGGCGTAAATGGAGTTGGTAAAAATATTAAAGAAGATCAAC 312  
  
 LysAlaIleValSerLysLysAsnLysAspIleValThrValAlaAsnAlaValPheValLys 98  
 AAGGCCATCGTCTCCAAGAAGAATAAAGACATTGTGACAGTGGCTAACGCCGTGTTTGTAAAG 375  
  
 AsnAlaSerGluIleGluValProPheValThrArgAsnLysAspValPheGlnCysGluVal 119  
 AATGCCTCTGAAATTGAAGTGCCCTTTTGTACAAAGGAACAAAGATGTGTCCAGTGTGAGGTC 438  
  
 ArgAsnValAsnPheGluAspProAlaSerAlaCysAspSerIleAsnAlaTrpValLysAsn 140  
 CGGAATGTGAACTTTGAGGATCCAGCCTCTGCCTGTGATTCCATCAATGCATGGGTAAAAAC 501  
  
 GluThrArgAspMetIleAspAsnLeuLeuSerProAspLeuIleAspGlyValLeuThrArg 161  
 GAAACCAGGGATATGATTGACAATCTGCTGTCCCAGATCTTATTGATGGTGTGCTCACCAGA 564  
  
 LeuValLeuValAsnAlaValTyrPheLysGlyLeuTrpLysSerArgPheGlnProGluAsn 182  
 CTGGTCCTCGTCAACGCAGTGTATTTCAGGGTCTGTGGAATCACGGTCCAACCCGAGAAG 627  
  
 ThrLysLysArgThrPheValAlaAlaAspGlyLysSerTyrGlnValProMetLeuAlaGln 203  
 ACAAAGAAACGCACTTTTCGTGGCAGCCGACGGGAAATCCTATCAAGTGCCAATGCTGGCCCCAG 690  
  
 LeuSerValPheArgCysGlySerThrSerAlaProAsnAspLeuTrpTyrAsnPheIleGlu 224  
 CTCTCCGTGTTCCGGTGTGGGTCGACAAGTGCCCCAATGATTATGGTACAACTTCATTGAA 753  
  
 LeuProTyrHisGlyGluSerIleSerMetLeuIleAlaLeuProThrGluSerSerThrPro 245  
 CTGCCCTACCACGGGGAAAGCATCAGCATGCTGATTGCACTGCCGACTGACAGCTCCACTCCG 816  
  
 LeuSerAlaIleIleProHisIleSerThrLysThrIleAspSerTrpMetSerIleMetVal 266  
 CTGTCTGCCATCATCCACACATCAGCACCAAGACCATAGACAGCTGGATGAGCATCATGGTG 879  
  
 ProLysArgValGlnValIleLeuProLysPheThrAlaValAlaGlnThrAspLeuLysGlu 287  
 CCCAAGAGGGTGCAGGTGATCCTGCCCAAGTTCACAGCTGTAGCACAACAGATTGAAGGAG 942



ProLeuLysValLeuGlyIleThrAspMetPheAspSerSerLysAlaAsnPheAlaLysIle 308  
 CCGCTGAAAGTTCCTGGCATTACTGACATGTTTGATTTCATCAAAGGCAAATTTTGCAAAAATA 1005

ThrX<sub>2</sub>-SerGluAsnLeuHisValSerHisIleLeuGlnLysAlaLysIleGluValSerGlu 329  
 ACAWGGTCAGAAAACCTCCATGTTTCTCATATCTTGCAAAAAGCAAAAATTGAAGTCAGTGAA 1068

AspGlyThrLysAlaSerAlaAlaThrThrAlaIleLeuIleAlaArgSerSerProProTrp 350  
 GATGGAACCAAAGCTTCAGCAGCAACAACTGCAATTCTCATTGCAAGATCATCGCCTCCCTGG 1131

PheIleValAspArgProPheLeuPhePheIleArgHisAsnProThrGlyAlaValLeuPhe 371  
 TTTATAGTAGACAGACCTTTTCTGTTTTTCATCCGACATAATCCTACAGGTGCTGTGTATTTC 1194

MetGlyGlnIleAsnLysPro  
 ATGGGGCAGATAAAACAAACCCTGAAGACTATACAAAAGAAACCATGCAAAGCAACGACTACTT 1257

TGC-Z<sub>4</sub>

(IV),

wherein W is A or ACAG, X<sub>2</sub> is Arg or Thr-Gly and Z<sub>3</sub> and Z<sub>4</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-standard DNA consisting of a DNA of formula IV and of a complementary DNA thereto, that complementary DNA itself, a mutant thereof, wherein one or more nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.

22. A DNA according to claim 20 of the formula III, wherein Y<sub>1</sub> to Y<sub>22</sub>, Z<sub>1</sub> and Z<sub>2</sub> have the meaning given under formula III, a double-stranded DNA consisting of a DNA of formula III and of a complementary DNA thereto, and that complementary DNA itself.

23. A DNA according to claim 21 of the formula IV, wherein W is A or ACAG, X<sub>2</sub> is Arg or Thr-Gly and Z<sub>3</sub> and Z<sub>4</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-stranded DNA consisting of a DNA of formula IV and of a complementary DNA thereto, and that complementary DNA itself.

24. A DNA according to claim 21 or 23 of the formula IV, wherein W is A and X<sub>2</sub> is Arg.

25. A DNA according to claim 21 or 23 of the formula IV, wherein W is ACAG and X<sub>2</sub> is Thr-Gly.

26. A DNA fragment according to claim 19, 20 or 21 comprising at least 15 bases.

27. A DNA according to claim 19, which hybridizes with a DNA of formula IV as defined in claim 21 or with a DNA complementary to the DNA of formula IV.

28. A DNA according to claim 19 of the formula

-1 1

MetAsnTrpHisPheProPhePheIleLeuThrThrValThrLeuSerSerValTyrSer 1  
 Z<sub>5</sub>-ATGAATTGGCAATTTCCCTTCTTCATCTTGACCACAGTGACTTTATCCTCTGTGTACTCC 60

GlnLeuAsnSerLeuSerLeuGluGluLeuGlySerAspThrGlyIleGlnValPheAsn 21  
 CAGCTCAACTCTCTGTCACTCGAGGAAGTGGCTCTGACACAGGGATCCAGGTTTTCAAT 120

GlnIleIleLysSerGlnProHisGluAsnValValIleSerProHisGlyIleAlaSer 41  
 CAGATCATCAAATCACAGCCTCATGAGAAGTTGTCAATTTCTCCGCACGGGATTGCGTCC 180

IleLeuGlyMetLeuGlnLeuGlyAlaAspGlyArgThrLysLysGlnLeuSerThrVal 61  
 ATCTTGGGCATGCTGCAGCTGGGGGCTGACGGCAGGACGAAGAAGCAGCTCTCAACGGTG 240

MetArgTyrAsnValAsnGlyValGlyLysValLeuLysLysIleAsnLysAlaIleVal 81  
 ATGCGATACAATGTGAACGGAGTCGAAAAGTGCTGAAGAAGATCAACAAGGCTATAGTC 300

SerLysLysAsnLysAspIleValThrValAlaAsnAlaValPheValArgAsnGlyPhe 101  
 TCCAAAAGAATAAAGACATAGTGACCGTGGCCAATGCTGTGTTTGICAGGAATGGCTTT 360

LysValGluValProPheAlaAlaArgAsnLysGluValPheGlnCysGluValGlnSer 121  
 AAAGTGGAAGTGCCTTTTGCAGCAAGGAACAAAGAGGTGTTTCAGTGTGAAGTACACAGT 420

ValAsnPheGlnAspProAlaSerAlaCysAspAlaIleAsnPheTrpValLysAsnGlu 141  
 GTGAACCTCCAGGACCCGGCCTCTGCTTGTGATGCCATCAATTTTGGGTCAAAAATGAG 480  
  
 ThrArgGlyMetIleAspAsnLeuLeuSerProAsnLeuIleAspSerAlaLeuThrLys 161  
 ACGAGGGGCATGATTGACAACCTACTTTCCCAAATCTGATCGATAGTGTCTTACCAA 540  
  
 LeuValLeuValAsnAlaValTyrPheLysGlyLeuTrpLysSerArgPheGlnProGlu 181  
 CTGGTCCTCGTTAAGCAGTGTATTTCAAGGGTTGTGAAATCCCGTTTCAACCTGAG 600  
  
 AsnThrLysLysArgThrPheValAlaGlyAspGlyLysSerTyrGlnValProMetLeu 201  
 AACACGAAGAAACGGACCTTCGTGGCAGGTGATGAAAATCCTACCAAGTACCCATGCTA 660  
  
 AlaGlnLeuSerValPheArgSerGlySerThrLysThrProAsnGlyLeuTrpTyrAsn 221  
 GCCCAGCTCTCCGTGTTCCGCTCTGGGTCTACCAAACCCCAAATGGCTTATGGTACAAC 720  
  
 PheIleGluLeuProTyrHisGlyGluSerIleSerMetLeuIleAlaLeuProThrGlu 241  
 TTCATTGAGCTACCCTACCATGGTGAGAGCATCAGCATGTTGATCGCCCTGCCAACAGAG 780  
  
 SerSerThrProLeuSerAlaIleIleProHisIleSerThrLysThrIleAsnSerTrp 261  
 AGCTCCACCCCACTGTCCGCCATCATCCCTCACATCAGTACCAAGACCATCAATAGCTGG 840  
  
 MetAsnThrMetValProLysArgMetGlnLeuValLeuProLysPheThrAlaLeuAla 281  
 ATGAACACCATGGTACCCAAGAGGATGCAGCTGGTCCTGCCCAAGTTCACAGCTCTGGCA 900  
  
 GlnThrAspLeuLysGluProLeuLysAlaLeuGlyIleThrGluMetPheGluProSer 301  
 CAAACAGATCTGAAGGAGCCACTGAAAGCCCTTGGCATTACTGAGATCTTTGAACCGTCA 960  
  
 LysAlaAsnPheAlaLysIleThrArgSerGluSerLeuHisValSerHisIleLeuGln 321  
 AAGGCAAATTTTGCAAAAATAACAAGGTCAGAGAGCCTTCACGTCTCTCACATCTTGCAG 1020  
  
 LysAlaLysIleGluValSerGluAspGlyThrLysAlaAlaValValThrThrAlaIle 341  
 AAAGCAAAAATTGAAGTCAGCGAAGATGGGACCAAAGCCGCAGTAGTACAACCTGCAATC 1080  
  
 LeuIleAlaArgSerSerProProTrpPheIleValAspArgProPheLeuPheCysIle 361  
 CTAATTGCAAGGTCATCGCCTCCCTGGTTTATAGTAGACAGGCCTTTCCTGTTCTGCATC 1140

ArgHisAsnProThrGlyAlaIleLeuPheLeuGlyGlnValAsnLysPro  
 CGACACAATCCACAGGTGCCATCTTGTTCCTGGGGCAGGTGAACAAGCCCTGA-Z<sub>6</sub>

5

(V),

- wherein Z<sub>5</sub> and Z<sub>6</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-stranded DNA consisting of a DNA of formula V and of a complementary DNA thereto, that complementary DNA itself, a mutant thereof, wherein one or more nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.
29. A RNA coding for a human GdNPF of formula I or for rat GdNPF, a mutant thereof, wherein one or more nucleotides are mutated, or a fragment of such RNA comprising at least 15 nucleotides.
30. A RNA according to claim 29 of formula III, wherein Y<sub>1</sub> to Y<sub>22</sub>, Z<sub>1</sub> and Z<sub>2</sub> have the meaning given under formula III in claim 20, except that RNA residues replace DNA residues and U replaces T.
31. A RNA according to claim 29 or 30 of formula IV, wherein W, Z<sub>3</sub> and Z<sub>4</sub> have the meaning given under formula IV in claim 21 except that RNA residues replace DNA residues and U replaces T.
32. A RNA according to claim 29 of formula V, wherein Z<sub>5</sub> and Z<sub>6</sub> have the meaning given under formula V in claim 28 except that RNA residues replace DNA residues and U replaces T.
33. A process for the preparation of DNAs coding for GdNPF, mutants thereof, DNAs coding for related polypeptides retaining neurite-promoting activity and fragments of such DNA comprising culturing a transformed host and isolating the desired DNA therefrom or synthesizing it by nucleotide condensation.
34. A process according to claim 33, comprising the steps of
- isolating poly(A) messenger RNA (mRNA) from glial cells, optionally enriching mRNA coding for GdNPF or fragments thereof and preparing single-stranded DNA complementary to that mRNA and therefrom double-stranded complementary DNA (ds cDNA), or
  - isolating genomic DNA from suitable cells and selecting the desired DNA using a DNA probe, and
  - incorporating ds cDNA of step a) or ds DNA of step b) into an appropriate expression vector.
  - transforming an appropriate host with the obtained hybrid vector,
  - selecting the transformed hosts which contain GdNPF DNA or fragments thereof from hosts containing no GdNPF DNA or fragments thereof, and
  - isolating the desired DNA.
35. A process according to claim 33, characterized in that an oligonucleotide is condensed with a mono- or oligonucleotide by chemical or enzymatic condensation.
36. A process according to claim 34, characterized in that in step a) the mRNA is isolated from the human glioma cell line LN-340, which has been deposited at the "Collection Nationale de Cultures de Microorganismes", Institut Pasteur, Paris, on February 5, 1986 under the number I-518.
37. A hybrid vector comprising a DNA coding for GdNPF, related peptides or fragments thereof, operatively linked to an expression control sequence.
38. A hybrid vector according to claim 37 derived from plasmid pBR322.
39. A hybrid vector according to claim 37 derived from plasmid pUC9.
40. A host cell transformed with a hybrid vector according to claims 37, 38 or 39.
41. A host cell according to claim 40 which is a cell of an *Escherichia coli* strain.
42. A host cell according to claim 40 or 41 which is a cell of the strain *E. coli* HB 101.
43. A pharmaceutical preparation containing a therapeutically effective amount of a GdNPF, a related polypeptide or a fragment thereof retaining neurite-promoting activity.
44. Use of a GdNPF, a related polypeptide or a fragment thereof retaining neurite-promoting activity for the manufacture of pharmaceutical preparations.

Claims for the following contracting states: AT, ES, GR

- A process for the preparation of essentially pure human glia-derived neurite-promoting factor (GdNPF), related polypeptides or fragments thereof retaining neurite-promoting activity, characterized in that the desired compound is isolated from cells producing it or is synthesized by condensation reactions.
- A process according to claim 1, comprising the steps of
  - isolating a DNA coding for GdNPF or a fragment thereof from a cDNA library of glial cells or a genomic DNA library and optionally mutating it, or chemically synthesizing such a DNA,
  - incorporating the DNA into an appropriate expression vector,
  - transferring the obtained hybrid vector into a recipient host,
  - selecting the transformed host from untransformed hosts by culturing under conditions under which only the transformed host survives,
  - culturing the transformed host under conditions which allow expression of the heterologous polypeptide, and

f) isolating the human GdNPF, related peptide, or fragment thereof.

3. A process according to claim 1, characterized in that a N-protected amino acid is coupled to a suitable resin, the protecting group is removed, a second N-protected amino acid is condensed with the amino group of the first amino acid, the cycle of deprotection/condensation with the next N-protected amino acid is repeated until the peptide residue of the desired composition is complete, and finally this peptide residue is cleaved from the resin and deprotected.

4. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare human GdNPF of the formula

X<sub>1</sub>-Ser-His-Phe-Asn-Pro-Leu-Ser-Leu-Glu-Glu-Leu-Gly-Ser-Asn-Thr-Gly- 16  
 Ile-Gln-Val-Phe-Asn-Gln-Ile-Val-Lys-Ser-Arg-Pro-His-Asp-Asn-Ile- 32  
 Val-Ile-Ser-Pro-His-Gly-Ile-Ala-Ser-Val-Leu-Gly-Met-Leu-Gln-Leu- 48  
 Gly-Ala-Asp-Gly-Arg-Thr-Lys-Lys-Gln-Leu-Ala-Met-Val-Met-Arg-Tyr- 64  
 Gly-Val-Asn-Gly-Val-Gly-Lys-Ile-Leu-Lys-Lys-Ile-Asn-Lys-Ala-Ile- 80  
 Val-Ser-Lys-Lys-Asn-Lys-Asp-Ile-Val-Thr-Val-Ala-Asn-Ala-Val-Phe- 96  
 Val-Lys-Asn-Ala-Ser-Glu-Ile-Glu-Val-Pro-Phe-Val-Thr-Arg-Asn-Lys- 112  
 Asp-Val-Phe-Gln-Cys-Glu-Val-Arg-Asn-Val-Asn-Phe-Glu-Asp-Pro-Ala- 128  
 Ser-Ala-Cys-Asp-Ser-Ile-Asn-Ala-Trp-Val-Lys-Asn-Glu-Thr-Arg-Asp- 144  
 Met-Ile-Asp-Asn-Leu-Leu-Ser-Pro-Asp-Leu-Ile-Asp-Gly-Val-Leu-Thr- 160  
 Arg-Leu-Val-Leu-Val-Asn-Ala-Val-Tyr-Phe-Lys-Gly-Leu-Trp-Lys-Ser- 176  
 Arg-Phe-Gln-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe-Val-Ala-Ala-Asp- 192  
 Gly-Lys-Ser-Tyr-Gln-Val-Pro-Met-Leu-Ala-Gln-Leu-Ser-Val-Phe-Arg- 208  
 Cys-Gly-Ser-Thr-Ser-Ala-Pro-Asn-Asp-Leu-Trp-Tyr-Asn-Phe-Ile-Glu- 224  
 Leu-Pro-Tyr-His-Gly-Glu-Ser-Ile-Ser-Met-Leu-Ile-Ala-Leu-Pro-Thr- 240  
 Glu-Ser-Ser-Thr-Pro-Leu-Ser-Ala-Ile-Ile-Pro-His-Ile-Ser-Thr-Lys- 256  
 Thr-Ile-Asp-Ser-Trp-Met-Ser-Ile-Met-Val-Pro-Lys-Arg-Val-Gln-Val- 272  
 Ile-Leu-Pro-Lys-Phe-Thr-Ala-Val-Ala-Gln-Thr-Asp-Leu-Lys-Glu-Pro- 288  
 Leu-Lys-Val-Leu-Gly-Ile-Thr-Asp-Met-Phe-Asp-Ser-Ser-Lys-Ala-Asn- 304  
 Phe-Ala-Lys-Ile-Thr-X<sub>2</sub>-Ser-Glu-Asn-Leu-His-Val-Ser-His-Ile-Leu- 320  
 Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala-Ser-Ala- 336  
 Ala-Thr-Thr-Ala-Ile-Leu-Ile-Ala-Arg-Ser-Ser-Pro-Trp-Phe-Ile- 352  
 Val-Asp-Arg-Pro-Phe-Leu-Phe-Phe-Ile-Arg-His-Asn-Pro-Thr-Gly-Ala- 368  
 Val-Leu-Phe-Met-Gly-Gln-Ile-Asn-Lys-Pro 378

(I),

optionally glycosylated, wherein Cys is optionally in the disulfide form, X<sub>1</sub> is hydrogen, acyl, the peptide residue of the formula

-19                      -15                      -10                      -5  
 Met-Asn-Trp-His-Leu-Pro-Leu-Phe-Leu-Leu-Ala-Ser-Val-Thr-Leu-Pro-Ser-

-1  
 Ile-Cys-

(II)

or a fragment of the residue of formula II comprising between 1 and 18 amino acids from the carboxyl end, optionally in acylated form, and X<sub>2</sub> is Arg or Thr-Gly, related polypeptides retaining neurite-promoting activity, wherein one or more single amino acids in the compound of the formula I are replaced by other amino acids, and fragments of the compound of the formula I comprising at least 10 consecutive amino acids selected from the amino acid chain between the amino acid 29 and amino acid 378 and optionally one or more other amino acids.

5. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare human GdNPF of the formula I, wherein Cys is optionally in the disulfide form and X<sub>1</sub> is hydrogen, acetyl, the peptide residue of the formula II or a fragment of the residue of formula II comprising between 1 and 18 amino acids from the carboxyl end.

6. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare human GdNPF of the formula I, wherein Cys is optionally in the disulfide form and X<sub>1</sub> is hydrogen, the peptide residue of the formula II, the fragment comprising the amino acids -18 to -1 of the formula II, Pro-Ser-Ile-Cys-, Ser-Ile-Cys-, Ile-Cys-, or Cys-.

7. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare human GdNPF of formula I, wherein X<sub>2</sub> is Arg.

8. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare human GdNPF of formula I, wherein X<sub>2</sub> is Thr-Gly.

9. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a GdNPF-related polypeptide of formula I, wherein X<sub>1</sub> and X<sub>2</sub> have the meaning given in claim 4 and wherein one, two, three or four single amino acids are replaced by other amino acids.

10. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to

prepare a fragment comprising at least 10 consecutive amino acids of the compound of the formula I, wherein X<sub>2</sub> is Arg or Thr-Gly, selected from the amino acid chain between the amino acid 29 and amino acid 378, and optionally one or more other amino acids.

11. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment comprising amino acids 2 to 378, 3 to 378, 4 to 378, 5 to 378, 6 to 378, or 7 to 378 of the compound of the formula I, wherein X<sub>2</sub> is Arg or Thr-Gly.

12. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment comprising 10 to 50 consecutive amino acids of formula I, wherein X<sub>2</sub> is Arg, including <sup>310</sup>Arg and <sup>311</sup>Ser and/or <sup>345</sup>Arg and <sup>348</sup>Ser and optionally one, two or three other amino acids.

13. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment comprising 10 to 50 consecutive amino acids of formula I including amino acids selected from the amino acid chain 72 to 96, 134 to 146, 159 to 195 or 314 to 378, and optionally one, two or three other amino acids.

14. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment of the formula Gln-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala.

15. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment of the formula His-Lys-Ala-Lys-Ile-Glu-Val-Ser-Glu-Asp-Gly-Thr-Lys-Ala.

16. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment of the formula Arg-Ser-Ser-Pro-Trp-Phe-Ile-Val-Asp-Ser-Phe.

17. A process according to claim 1, 2 or 3, characterized in that the starting material is so chosen as to prepare a fragment of the formula Lys-Ser-Arg-Phe-Gln-Pro-Glu-Asn-Thr-Lys-Lys-Arg-Thr-Phe.

18. A process for the preparation of DNAs coding for GdNPF, mutants thereof, DNAs coding for related polypeptides retaining neurite-promoting activity and fragments of such DNA comprising culturing a transformed host and isolating the desired DNA therefrom or synthesizing it by nucleotide condensation.

19. A process according to claim 18, comprising the steps of

a) isolating poly(A) messenger RNA (mRNA) from glial cells, optionally enriching mRNA coding for GdNPF or fragments thereof and preparing single-stranded DNA complementary to that mRNA and therefrom double-stranded complementary DNA (ds cDNA), or

b) isolating genomic DNA from suitable cells and selecting the desired DNA using a DNA probe, and

c) incorporating ds cDNA of step a) or ds DNA of step b) into an appropriate expression vector,

d) transforming an appropriate host with the obtained hybrid vector,

e) selecting the transformed hosts which contain GdNPF DNA or fragments thereof from hosts containing no GdNPF DNA or fragments thereof, and

f) isolating the desired DNA.

20. A process according to claim 18, characterized in that an oligonucleotide is condensed with a mono- or oligonucleotide by chemical or enzymatic condensation.

21. A process according to claim 19, characterized in that in step a) the mRNA is isolated from the human glioma cell line LN-340, which has been deposited at the "Collection Nationale de Cultures de Microorganismes", Institut Pasteur, Paris, on February 5, 1986 under the number I-518.

22. A process according to claim 18, 19 or 20, characterized in that the starting material is so chosen as to prepare a DNA of the formula Z<sub>1</sub>-Y<sub>13</sub>-Y<sub>3</sub>-Y<sub>18</sub>-Y<sub>9</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>14</sub>-Y<sub>11</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>20</sub>-Y<sub>17</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>16</sub>-Y<sub>10</sub>-Y<sub>5</sub>-Y<sub>16</sub>-Y<sub>9</sub>-Y<sub>14</sub>-Y<sub>3</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>11</sub>-Y<sub>7</sub>-Y<sub>7</sub>-Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>16</sub>-Y<sub>3</sub>-Y<sub>17</sub>-Y<sub>8</sub>-Y<sub>10</sub>-Y<sub>6</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>3</sub>-Y<sub>6</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>12</sub>-Y<sub>16</sub>-Y<sub>2</sub>-Y<sub>15</sub>-Y<sub>9</sub>-Y<sub>4</sub>-Y<sub>3</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>10</sub>-Y<sub>16</sub>-Y<sub>15</sub>-Y<sub>9</sub>-Y<sub>8</sub>-Y<sub>10</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>13</sub>-Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>2</sub>-Y<sub>13</sub>-Y<sub>20</sub>-Y<sub>3</sub>-Y<sub>8</sub>-Y<sub>20</sub>-Y<sub>8</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>12</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>16</sub>-Y<sub>12</sub>-Y<sub>12</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>4</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>17</sub>-Y<sub>20</sub>-Y<sub>1</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>20</sub>-Y<sub>12</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>7</sub>-Y<sub>10</sub>-Y<sub>7</sub>-Y<sub>20</sub>-Y<sub>15</sub>-Y<sub>14</sub>-Y<sub>20</sub>-Y<sub>17</sub>-Y<sub>2</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>4</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>6</sub>-Y<sub>5</sub>-Y<sub>7</sub>-Y<sub>20</sub>-Y<sub>2</sub>-Y<sub>3</sub>-Y<sub>20</sub>-Y<sub>3</sub>-Y<sub>14</sub>-Y<sub>7</sub>-Y<sub>4</sub>-Y<sub>15</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>5</sub>-Y<sub>4</sub>-Y<sub>16</sub>-Y<sub>10</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>18</sub>-Y<sub>20</sub>-Y<sub>12</sub>-Y<sub>3</sub>-Y<sub>7</sub>-Y<sub>17</sub>-Y<sub>2</sub>-Y<sub>4</sub>-Y<sub>13</sub>-Y<sub>10</sub>-Y<sub>4</sub>-Y<sub>3</sub>-Y<sub>11</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>15</sub>-Y<sub>4</sub>-Y<sub>11</sub>-Y<sub>10</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>17</sub>-Y<sub>2</sub>-Y<sub>11</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>20</sub>-Y<sub>3</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>19</sub>-Y<sub>14</sub>-Y<sub>12</sub>-Y<sub>8</sub>-Y<sub>11</sub>-Y<sub>18</sub>-Y<sub>12</sub>-Y<sub>18</sub>-Y<sub>2</sub>-Y<sub>14</sub>-Y<sub>6</sub>-Y<sub>15</sub>-Y<sub>7</sub>-Y<sub>3</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>12</sub>-Y<sub>2</sub>-Y<sub>17</sub>-Y<sub>14</sub>-Y<sub>20</sub>-Y<sub>1</sub>-Y<sub>1</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>12</sub>-Y<sub>16</sub>-Y<sub>19</sub>-Y<sub>6</sub>-Y<sub>20</sub>-Y<sub>15</sub>-Y<sub>13</sub>-Y<sub>11</sub>-Y<sub>1</sub>-Y<sub>6</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>20</sub>-Y<sub>14</sub>-Y<sub>2</sub>-Y<sub>5</sub>-Y<sub>8</sub>-Y<sub>18</sub>-Y<sub>17</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>15</sub>-Y<sub>3</sub>-Y<sub>4</sub>-Y<sub>11</sub>-Y<sub>18</sub>-Y<sub>19</sub>-Y<sub>3</sub>-Y<sub>14</sub>-Y<sub>10</sub>-Y<sub>7</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>19</sub>-Y<sub>9</sub>-Y<sub>8</sub>-Y<sub>7</sub>-Y<sub>16</sub>-Y<sub>10</sub>-Y<sub>16</sub>-Y<sub>13</sub>-Y<sub>11</sub>-Y<sub>10</sub>-Y<sub>1</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>17</sub>-Y<sub>7</sub>-Y<sub>18</sub>-Y<sub>18</sub>-Y<sub>17</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>10</sub>-Y<sub>10</sub>-Y<sub>15</sub>-Y<sub>9</sub>-Y<sub>10</sub>-Y<sub>16</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>17</sub>-Y<sub>10</sub>-Y<sub>4</sub>-Y<sub>16</sub>-Y<sub>18</sub>-Y<sub>13</sub>-Y<sub>18</sub>-Y<sub>10</sub>-Y<sub>13</sub>-Y<sub>20</sub>-Y<sub>15</sub>-Y<sub>12</sub>-Y<sub>2</sub>-Y<sub>20</sub>-Y<sub>6</sub>-Y<sub>20</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>15</sub>-Y<sub>12</sub>-Y<sub>14</sub>-Y<sub>17</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>1</sub>-Y<sub>6</sub>-Y<sub>17</sub>-Y<sub>4</sub>-Y<sub>11</sub>-Y<sub>12</sub>-Y<sub>7</sub>-Y<sub>15</sub>-Y<sub>11</sub>-Y<sub>12</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>8</sub>-Y<sub>10</sub>-Y<sub>17</sub>-Y<sub>4</sub>-Y<sub>13</sub>-Y<sub>14</sub>-Y<sub>4</sub>-Y<sub>18</sub>-Y<sub>16</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>3</sub>-Y<sub>14</sub>-Y<sub>1</sub>-Y<sub>12</sub>-Y<sub>1</sub> 0-Y<sub>17</sub>-Y<sub>22</sub>-Y<sub>16</sub>-Y<sub>7</sub>-Y<sub>3</sub>-Y<sub>11</sub>-Y<sub>9</sub>-Y<sub>20</sub>-Y<sub>18</sub>-Y<sub>9</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>6</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>12</sub>-Y<sub>10</sub>-Y<sub>7</sub>-Y<sub>20</sub>-Y<sub>16</sub>-Y<sub>7</sub>-Y<sub>4</sub>-Y<sub>8</sub>-Y<sub>17</sub>-Y<sub>12</sub>-Y<sub>1</sub>-Y<sub>16</sub>-Y<sub>1</sub>-Y<sub>1</sub>-Y<sub>17</sub>-Y<sub>17</sub>-Y<sub>1</sub>-Y<sub>10</sub>-Y<sub>11</sub>-Y<sub>10</sub>-Y<sub>1</sub>-Y<sub>2</sub>-Y<sub>16</sub>-Y<sub>16</sub>-Y<sub>15</sub>-Y<sub>15</sub>-Y<sub>18</sub>-Y<sub>14</sub>-Y<sub>10</sub>-Y<sub>20</sub>-Y<sub>4</sub>-Y<sub>2</sub>-Y<sub>15</sub>-Y<sub>14</sub>-Y<sub>11</sub>-Y<sub>14</sub>-Y<sub>10</sub>-Y<sub>2</sub>-Y<sub>9</sub>-Y<sub>3</sub>-Y<sub>15</sub>-Y<sub>17</sub>-Y<sub>8</sub>-Y<sub>1</sub>-Y<sub>20</sub>-Y<sub>11</sub>-Y<sub>14</sub>-Y<sub>13</sub>-Y<sub>8</sub>-Y<sub>6</sub>-Y<sub>10</sub>-Y<sub>3</sub>-Y<sub>12</sub>-Y<sub>15</sub>-Y<sub>21</sub>-Z<sub>2</sub>

(III),

wherein

Y<sub>1</sub> codes for alanine (Ala) and is GCT, GCC, GCA or GCG,

Y<sub>2</sub> codes for arginine (Arg) and is CGT, CGC, CGA, CGG, AGA or AGG,

Y<sub>3</sub> codes for asparagine (Asn) and is AAT or AAC,

Y<sub>4</sub> codes for aspartic acid (Asp) and is GAT or GAC,

Y<sub>5</sub> codes for cysteine (Cys) and is TGT or TGC,

Y<sub>6</sub> codes for glutamine (Gln) and is CAA or CAG,

Y<sub>7</sub> codes for glutamic acid (Glu) and is GAA or GAG,  
 Y<sub>8</sub> codes for glycine (Gly) and is GGT, GGC, GGA or GGG,  
 Y<sub>9</sub> codes for histidine (His) and is CAT or CAC,  
 Y<sub>10</sub> codes for isoleucine (Ile) and is ATT, ATC or ATA,  
 Y<sub>11</sub> codes for leucine (Leu) and is TTA, TTG, CTT, CTC, CTA or CTG,  
 Y<sub>12</sub> codes for lysine (Lys) and is AAA or AAG, 5  
 Y<sub>13</sub> codes for methionine (Met) and is ATG,  
 Y<sub>14</sub> codes for phenylalanine (Phe) and is TTT or TTC,  
 Y<sub>15</sub> codes for proline (Pro) and is CCT, CCC, CCA or CCG,  
 Y<sub>16</sub> codes for serine (Ser) and is TCT, TCC, TCA, TCG, AGT or AGC, 10  
 Y<sub>17</sub> codes for threonine (Thr) and is ACT, ACC, ACA or ACG,  
 Y<sub>18</sub> codes for tryptophan (Trp) and is TGG,  
 Y<sub>19</sub> codes for tyrosine (Tyr) and is TAT or TAC,  
 Y<sub>20</sub> codes for valine (Val) and is GTT, GTC, GTA or GTG,  
 Y<sub>21</sub> is a stop codon TAA, TAG or TGA, 15  
 Y<sub>22</sub> is Y<sub>2</sub> or Y<sub>17</sub>-Y<sub>9</sub>,  
 Z<sub>1</sub> is a flanking DNA residue of 12 nucleotides or more containing a promoter sequence,  
 Z<sub>2</sub> is absent or a flanking DNA residue of one or more nucleotides, and Z<sub>1</sub> and Z<sub>2</sub> are optionally linked,  
 a double-stranded DNA consisting of a DNA of formula III and of a complementary DNA thereto, that  
 complementary DNA itself, a mutant thereof, wherein one or more nucleotides are mutated, and 20  
 fragments of such DNA comprising at least 15 nucleotides.  
 23. A process according to claim 18, 19 or 20, characterized in that the starting material is so chosen as  
 to prepare a DNA of the formula

MetAsnTrpHisLeuProLeuPheLeuLeuAlaSer -8 25  
 Z<sub>3</sub>-CGGTCGTCCTTGGTGGAAGTAACCATGAAGTGGCATCTCCCCCTCTTCCTCTTGGCCTCT 60  
 -1 1  
 ValThrLeuProSerIleCysSerHisPheAsnProLeuSerLeuGluGluLeuGlySerAsn 14 30  
 GTGACGCTGCCTTCCATCTGCTCCCACTTCAATCCTCTGTCTCTCGAGGAAGTGGCTCCAAC 123  
 ThrGlyIleGlnValPheAsnGlnIleValLysSerArgProHisAspAsnIleValIleSer 35 35  
 ACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCCTCATGACAACATCGTGATCTCT 186  
 ProHisGlyIleAlaSerValLeuGlyMetLeuGlnLeuGlyAlaAspGlyArgThrLysLys 56 40  
 CCCCATGGGATTGCGTCGGTCTGGGGATGCTTCAGCTGGGGGGGACGGCAGGACCAAGAAG 249  
 GlnLeuAlaMetValMetArgTyrGlyValAsnGlyValGlyLysIleLeuLysLysIleAsn 77 45  
 CAGCTCGCCATGGTGATGAGATACGGCGTAAATGGAGTTGGTAAATATTAAAGAAGATCAAC 312  
 LysAlaIleValSerLysLysAsnLysAspIleValThrValAlaAsnAlaValPheValLys 98 50  
 AAGGCCATCGTCTCCAAGAAGATAAAGACATTGTGACAGTGGCTAACGCCGTGTTTGTAAAG 375  
 AsnAlaSerGluIleGluValProPheValThrArgAsnLysAspValPheGlnCysGluVal 119 55  
 AATGCCCTCTGAAATTGAAGTGCCCTTTTGTACAAGGAACAAAGATGTGTCCAGTGTGAGGTC 438  
 ArgAsnValAsnPheGluAspProAlaSerAlaCysAspSerIleAsnAlaTrpValLysAsn 140 60  
 CGGAATGTGAAGTTTGAGGATCCAGCCTCTGCCTGTGATTCCATCAATGCATGGGTTAAAAAC 501

GluThrArgAspMetIleAspAsnLeuLeuSerProAspLeuIleAspGlyValLeuThrArg 161  
 GAAACCAGGGATATGATTGACAATCTGCTGTCCCAGATCTTATTGATGGTGTGCTCACCAGA 564  
  
 LeuValLeuValAsnAlaValTyrPheLysGlyLeuTrpLysSerArgPheGlnProGluAsn 182  
 CTGGTCCTCGTCAACCCAGTGTATTTCAAGGGTCTGTGGAAATCACGGTTCCAACCCGAGAAC 627  
  
 ThrLysLysArgThrPheValAlaAlaAspGlyLysSerTyrGlnValProMetLeuAlaGln 203  
 ACAAAGAAACGCACTTTCGTGGCAGCCGACGGGAAATCCTATCAAGTGCCAATGCTGGCCCAG 690  
  
 LeuSerValPheArgCycGlySerThrSerAlaProAsnAspLeuTrpTyrAsnPheIleGlu 224  
 CTCTCCGTGTTCCGGTGTGGTTCGACAAGTGCCCCAATGATTTATGGTACAACCTTCATTGAA 753  
  
 LeuProTyrHisGlyGluSerIleSerMetLeuIleAlaLeuProThrGluSerSerThrPro 245  
 CTGCCCTACCAACGGGAAAGCATCAGCATGCTGATTGCACTGCCGACTGAGAGCTCCACTCCG 816  
  
 LeuSerAlaIleIleProHisIleSerThrLysThrIleAspSerTrpMetSerIleMetVal 266  
 CTGTCTGCCATCATCCACACATCAGCACCAAGACCATAGACAGCTGGATGAGCATCATGGTG 879  
  
 ProLysArgValGlnValIleLeuProLysPheThrAlaValAlaGlnThrAspLeuLysGlu 287  
 CCCAAGAGGGTGCAGGTGATCCTGCCCCAAGTTCACAGCTGTAGCACAAACAGATTTGAAGGAG 942  
  
 ProLeuLysValLeuGlyIleThrAspMetPheAspSerSerLysAlaAsnPheAlaLysIle 308  
 CCGCTGAAAGTTCTTGGCATTACTGACATGTTTGATTCATCAAAGGCAAATTTTGCAAAAATA 1005  
  
 ThrX<sub>2</sub>-SerGluAsnLeuHisValSerHisIleLeuGlnLysAlaLysIleGluValSerGlu 329  
 ACAWGGTCAGAAAACCTCCATGTTTCTCATATCTTGCAAAAAGCAAAAATTGAAGTCAGTGAA 1068  
  
 AspGlyThrLysAlaSerAlaAlaThrThrAlaIleLeuIleAlaArgSerSerProProTrp 350  
 GATGGAACCAAAGCTTCAGCAGCAACAACCTGCAATTCTCATTGCAAGATCATCGCCTCCCTGG 1131  
  
 PheIleValAspArgProPheLeuPhePheIleArgHisAsnProThrGlyAlaValLeuPhe 371  
 TTTATAGTAGACAGACCTTTTCTGTTTTTCATCCGACATAATCCTACAGGTGCTGTGTATTTC 1194



MetGlyGlnIleAsnLysPro

ATGGGGCAGATAAACAACCCCTGAAGAGTATACAAAAGAAACCATGCAAAGCAACGACTACTT 1257

TGC-Z<sub>4</sub>

(IV),

wherein W is A or ACAG, X<sub>2</sub> is Arg or Thr-Gly and Z<sub>3</sub> and Z<sub>4</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-stranded DNA consisting of a DNA of formula IV and of a complementary DNA thereto, that complementary DNA itself, a mutant thereof, wherein one or more nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.

24. A process according to claim 18, 19 or 21, characterized in that the starting material is so chosen as to prepare a DNA of the formula IV, wherein W is A and X<sub>2</sub> is Arg.

25. A process according to claim 18, 19 or 21, characterized in that the starting material is so chosen as to prepare a DNA of the formula IV, wherein W is ACAG and X<sub>2</sub> is Thr-Gly.

26. A process according to claim 18, 19 or 20, characterized in that the starting material is so chosen as to prepare a DNA, which hybridizes with a DNA of formula IV or with a DNA complementary to the DNA of formula IV.

27. A process according to claim 18, 19 or 20, characterized in that the starting material is so chosen as to prepare a DNA of the formula

-1 1

MetAsnTrpHisPheProPhePheIleLeuThrThrValThrLeuSerSerValTyrSer 1

Z<sub>5</sub>-ATGAATTGGCATTTCCTTCTTCATCTTGACCACAGTGACTTTATCCTCTGTGTACTCC 60

GlnLeuAsnSerLeuSerLeuGluGluLeuGlySerAspThrGlyIleGlnValPheAsn 21

CAGCTCAACTCTCTGTCACTCGAGGAAGTGGCTCTGACACAGGGATCCAGGTTTTCAAT 120

GlnIleIleLysSerGlnProHisGluAsnValValIleSerProHisGlyIleAlaSer 41  
 CAGATCATCAAATCACAGCCTCATGAGAACGTTGTCATTCTCCGCACGGGATTGCGTCC 180  
  
 IleLeuGlyMetLeuGlnLeuGlyAlaAspGlyArgThrLysLysGlnLeuSerThrVal 61  
 ATCTTGGGCATGCTGCAGCTGGGGGCTGACGGCAGGACGAAGAAGCAGCTCTCAACGGTG 240  
  
 MetArgTyrAsnValAsnGlyValGlyLysValLeuLysLysIleAsnLysAlaIleVal 81  
 ATGCCGATACAATCTGAACGGAGTCGGAAAAGTGCTGAAGAAGATCAACAAGGCTATAGTC 300  
  
 SerLysLysAsnLysAspIleValThrValAlaAsnAlaValPheValArgAsnGlyPhe 101  
 TCCAAAAAGAATAAAGACATAGTGACCGTGGCCAATGCTGTGTTTGTGAGGAATGGCTTT 360  
  
 LysValGluValProPheAlaAlaArgAsnLysGluValPheGlnCysGluValGlnSer 121  
 AAAGTGAAGTGCCTTTTGCAGCAAGGAACAAAGAGGTGTTTCAGTGGAAGTACAGAGT 420  
  
 ValAsnPheGlnAspProAlaSerAlaCysAspAlaIleAsnPheTrpValLysAsnGlu 141  
 GTGAAGTTCAGGACCCGGCCTCTGCTTGTGATGCCATCAATTTTGGGTCAAAAATGAG 480  
  
 ThrArgGlyMetIleAspAsnLeuLeuSerProAsnLeuIleAspSerAlaLeuThrLys 161  
 ACGAGGGGCATGATTGACAACCTACTTTCCCAATCTGATCGATAGTGTCTTACCAAA 540  
  
 LeuValLeuValAsnAlaValTyrPheLysGlyLeuTrpLysSerArgPheGlnProGlu 181  
 CTGGTCCTCGTTAACGCAGTGTATTCAAGGGTTTGTGGAAATCCCGGTTTCAACCTGAG 600  
  
 AsnThrLysLysArgThrPheValAlaGlyAspGlyLysSerTyrGlnValProMetLeu 201  
 AACACGAAGAAACGGACCTTCGTGGCAGGTGATGGAATCCTACCAAGTACCCATGCTA 660  
  
 AlaGlnLeuSerValPheArgSerGlySerThrLysThrProAsnGlyLeuTrpTyrAsn 221  
 GCCCAGCTCTCCGTGTTCCGCTCTGGGTCTACCAAAACCCAAATGGCTTATGGTACAAC 720  
  
 PheIleGluLeuProTyrHisGlyGluSerIleSerMetLeuIleAlaLeuProThrGlu 241  
 TTCATTGAGCTACCCTACCATGGTGAGAGCATCAGCATGTTGATCGCCCTGCCAACAGAG 780  
  
 SerSerThrProLeuSerAlaIleIleProHisIleSerThrLysThrIleAsnSerTrp 261  
 AGCTCCACCCCACTGTCCGCCATCATCCCTCACATCAGTACCAAGACCATCAATAGCTGG 840

MetAsnThrMetValProLysArgMetGlnLeuValLeuProLysPheThrAlaLeuAla 281  
 ATGAACACCATGGTACCCAAGAGGATGCAGCTGGTCCTGCCCAAGTTCACAGCTCTGGCA 900

GlnThrAspLeuLysGluProLeuLysAlaLeuGlyIleThrGluMetPheGluProSer 301  
 CAAACAGATCTGAAGGAGCCACTGAAAGCCCTTGGCATTACTGAGATCTTTGAACCGTCA 960

LysAlaAsnPheAlaLysIleThrArgSerGluSerLeuHisValSerHisIleLeuGln 321  
 AAGGCAAATTTTGCAAAAATAACAAGGTCAGAGAGCCTTCACGTCTCTCACATCTTGCA 1020

LysAlaLysIleGluValSerGluAspGlyThrLysAlaAlaValValThrThrAlaIle 341  
 AAAGCAAAAATTGAAGTCAGCGAAGATGGGACCAAAGCCGCAGTAGTGACAACGTCAATC 1080

LeuIleAlaArgSerSerProProTrpPheIleValAspArgProPheLeuPheCysIle 361  
 CTAATTGCAAGGTCATCGCCTCCCTGGTTTATAGTAGACAGGCCCTTTCCTGTTCTGCATC 1140

ArgHisAsnProThrGlyAlaIleLeuPheLeuGlyGlnValAsnLysPro  
 CGACACAATCCCACAGGTGCCATCTTGTTCTGGGGCAGGTGAACAAGCCCTGA-Z<sub>6</sub>

(V),

wherein Z<sub>5</sub> and Z<sub>6</sub>, independently, are absent or a flanking DNA residue of one or more nucleotides optionally linked, a double-stranded DNA consisting of a DNA of formula V and of a complementary DNA thereto, that complementary DNA itself, a mutant thereof, wherein one or more nucleotides are mutated, and fragments of such DNA comprising at least 15 nucleotides.

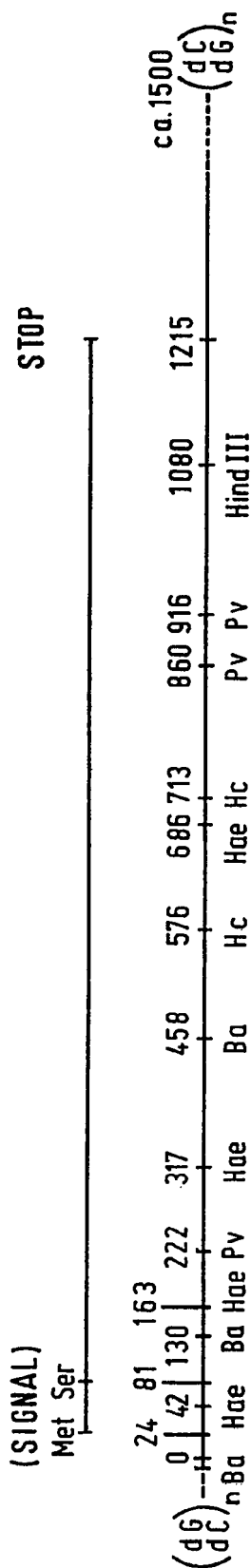
28. A process for the preparation of a RNA coding for a human GdNPF of formula I or for rat GdNPF, a mutant thereof, wherein one or more nucleotides are mutated, or a fragment of such RNA comprising at least 15 nucleotides, characterized in that it is isolated from glial cells.

29. A host cell transformed with a hybrid vector comprising a DNA coding for GdNPF, related peptides or fragments thereof operatively linked to an expression control sequence.

30. A host cell according to claim 29 which is a cell of an *Escherichia coli* strain.

31. A host cell according to claim 29 or 30 which is a cell of the strain *E. coli* HB 101.

32. A process for the preparation of a pharmaceutical composition, characterized in that human GdNPF, related polypeptides or fragments thereof retaining neurite-promoting activity are mixed with a pharmaceutically acceptable carrier.



Ba = BamHI  
 Hae = HaeIII  
 Hc = HincII  
 Pv = PvuII

0233838